

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 11:34:17 ; Search time 56 Seconds
(without alignments)
165.519 Million cell updates/sec

Title: US-09-913-325-5

Sequence: 1 atgtctgagagctcttc 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 segs, 220591566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/prodata/2/ina/5A COMB.seq:*
- 2: /cgn2_6/prodata/2/ina/5B COMB.seq:*
- 3: /cgn2_6/prodata/2/ina/6A COMB.seq:*
- 4: /cgn2_6/prodata/2/ina/6B COMB.seq:*
- 5: /cgn2_6/prodata/2/ina/6C COMB.seq:*
- 6: /cgn2_6/prodata/2/ina/6D COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	21	100.0	195	2	US-08-485-657A-14
C 2	21	100.0	195	4	US-09-366-380-14
C 3	21	100.0	195	5	PCT-US95-02303-14
C 4	21	100.0	1648	4	US-09-659-791A-3
C 5	21	100.0	1651	4	US-09-659-791A-13
C 6	21	100.0	7610	4	US-09-659-791A-12
C 7	19.4	92.4	181	2	US-08-485-657A-19
C 8	19.4	92.4	181	4	US-09-366-380-19
C 9	19.4	92.4	181	5	PCT-US95-02303-18
C 10	15.2	72.4	6671	1	US-08-280-443-1
C 11	15.2	72.4	6671	1	US-08-457-459-1
C 12	15.2	72.4	6671	1	US-08-555-678-1
C 13	15.2	72.4	6671	5	PCT-US95-02275-1
C 14	15.2	72.4	6756	1	US-08-151-574-31
C 15	15.2	72.4	6756	2	US-08-419-448-31
C 16	15.2	72.4	6756	4	US-09-233-510-31
C 17	14.8	70.5	1438	3	US-09-187-331-4
C 18	14.8	70.5	1438	4	US-09-470-946-4
C 19	14.8	70.5	3563	3	US-09-041-886-20
C 20	14.8	70.5	3596	2	US-08-779-801-5
C 21	14.8	70.5	3596	4	US-09-298-441-5
C 22	14.8	70.5	4403765	3	US-09-103-840A-2
C 23	14.8	70.5	4411529	3	US-09-103-840A-1
C 24	14.6	69.5	885	4	US-09-252-991A-2618
C 25	14.6	69.5	1080	4	US-09-252-991A-2217
C 26	14.6	69.5	1219	4	US-09-192-012-1
C 27	14.6	69.5	2139	4	US-09-252-991A-2295

C 28	14.6	69.5	2820	4	US-09-252-991A-2538
C 29	14.6	69.5	2820	5	PCT-US93-11725-1
C 30	14.6	69.5	2872	1	US-08-015-985-4
C 31	14.4	68.6	59	4	US-09-475-947A-52
C 32	14.4	68.6	494	4	US-09-702-705-45
C 33	14.4	68.6	494	4	US-09-736-457-45
C 34	14.4	68.6	2002	2	US-08-715-202A-3
C 35	14.4	68.6	2002	4	US-09-328-775-3
C 36	14.4	68.6	13205	4	US-09-835-811-3
C 37	14.2	67.6	331	3	US-09-060-756-310
C 38	14.2	67.6	331	4	US-09-670-314-310
C 39	14.2	67.6	511	4	US-09-389-681-443
C 40	14.2	67.6	511	4	US-09-620-405B-443
C 41	14.2	67.6	511	4	US-09-433-826B-443
C 42	14.2	67.6	511	4	US-09-404-287A-443
C 43	14.2	67.6	747	4	US-09-552-991A-16237
C 44	14.2	67.6	939	3	US-09-105-390-45
C 45	14.2	67.6	944	2	US-08-522-421-2

ALIGNMENTS

RESULT 1
US-08-485-657A-14/c
; Sequence 14, Application US/08485657A
; Patent No. 5942389
; GENERAL INFORMATION:
; APPLICANT: Kirschling, Deborah J
; APPLICANT: Gudkov, Andrei
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; TITLE OF INVENTION: with Sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,657A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5942389nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-485-657A-14

Query Match 100.0%; Score 21; DB 2; Length 195;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 21; Conservative 0; Mismatches 0; Gaps 0;

1 ATTGTCGAGACCGTCGTC 21

Db 153 ATTGTCTGAGACCGTCTGGTC 133

RESULT 2

US-09-366-380-14/c

Sequence 14, Application US/09366380

Patent No. 6541603

GENERAL INFORMATION:

APPLICANT: Kirschling, Deborah J

APPLICANT: Gudkov, Andrei

APPLICANT: Roninson, Igor B

TITLE OF INVENTION: Genes and Genetic Elements Associated

TITLE OF INVENTION: with Sensitivity to Cisplatin

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff

STREET: 300 South Wacker Drive, 32nd Floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/366,380

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/199,900

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: No. 6541603nan, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 93,354-N

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-913-0001

TELEFAX: 312-913-0002

TELEX:

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 195 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-09-366-380-14

Query Match 100.0%; Score 21; DB 4; Length 195;

Best Local Similarity 100.0%; Pred. No. 0.05;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGTCTGAGACCGTCTGGTC 21

Db 153 ATTGTCTGAGACCGTCTGGTC 133

RESULT 3

PCT-US95-02303-14/c

Sequence 14, Application PC/TUS9502303

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Genes and Genetic Elements Associated

TITLE OF INVENTION: with Sensitivity to Cisplatin

NUMBER OF SEQUENCES: 25

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/02303

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 195 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

PCT-US95-02303-14

Query Match 100.0%; Score 21; DB 5; Length 195;

Best Local Similarity 100.0%; Pred. No. 0.05;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGTCTGAGACCGTCTGGTC 21

Db 153 ATTGTCTGAGACCGTCTGGTC 133

RESULT 4

US-09-659-791A-3/c

Sequence 3, Application US/09659791A

Patent No. 6383808

GENERAL INFORMATION:

APPLICANT: Brett P. Monia

APPLICANT: Susan M. Preier

TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION

FILE REFERENCE: RTS-0156

CURRENT APPLICATION NUMBER: US/09/659,791A

CURRENT FILING DATE: 2000-09-11

NUMBER OF SEQ ID NOS: 90

SEQ ID NO 3

LENGTH: 1648

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (53)...(1402)

US-09-659-791A-3

Query Match 100.0%; Score 21; DB 4; Length 1648;

Best Local Similarity 100.0%; Pred. No. 0.072;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGTCTGAGACCGTCTGGTC 21

Db 139 ATTGTCTGAGACCGTCTGGTC 119

RESULT 5

US-09-659-791A-13/c

Sequence 13, Application US/09659791A

Patent No. 6383808

GENERAL INFORMATION:

APPLICANT: Brett P. Monia

APPLICANT: Susan M. Preier

TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION

FILE REFERENCE: RTS-0156

CURRENT APPLICATION NUMBER: US/09/659,791A

CURRENT FILING DATE: 2000-09-11

NUMBER OF SEQ ID NOS: 90

SEQ ID NO 13

LENGTH: 1651

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (199)...(1545)

US-09-659-791A-13

Query Match 100.0%; Score 21; DB 4; Length 1651;

Best Local Similarity 100.0%; Pred. No. 0.072;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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2Y      1 ATTGCTGAGACCGTCTGGTC 21
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      282 ATTGCTGAGACCGTCTGGTC 262
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Dbb

RESULT 6
US-09-659-791A-12/c
; Sequence 12, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 12
; LENGTH: 7610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 5461
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 5462
; OTHER INFORMATION: unknown
; OTHER INFORMATION: unknown
US-09-659-791A-12

Query Match 100.0%; Score 21; DB 4; Length 7610;
Best Local Similarity 100.0%; Pred. No. 0.093;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATTGCTGAGACCGTCTGGTC 21
      |||||
      5624 ATTGCTGAGACCGTCTGGTC 5604

Dbb

RESULT 7
US-08-485-657A-19/c
; Sequence 19, Application US/08485657A
; Patent No. 5942389
; GENERAL INFORMATION:
; APPLICANT: Kirschling, Deborah J
; APPLICANT: Gudkov, Andrei
; APPLICANT: Robinson, Igor B
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; TITLE OF INVENTION: with Sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,657A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5942389nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001

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Db 139 ATGGCTGAGACCGCTGCTGTC 119

RESULT 9

PCT-US95-02303-18/c

Sequence 18, Application PC/TUS9502303

GENERAL INFORMATION:

APPLICANT: Genes and Genetic Elements Associated

TITLE OF INVENTION: with Sensitivity to Cisplatin

NUMBER OF SEQUENCES: 25

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/02303

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 181 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

PCT-US95-02303-18

Query Match 92.4%; Score 19.4; DB 5; Length 181;

Best Local Similarity 95.2%; Pred. No. 0.34; 1; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 1;

Qy 1 ATTGCTGAGACCGCTGCTGTC 21

Db 139 ATGGCTGAGACCGCTGCTGTC 119

RESULT 10

US-08-280-443-1/c

Sequence 1, Application US/08280443

Patent No. 5643778

GENERAL INFORMATION:

APPLICANT: Nishikura, Kazuko

TITLE OF INVENTION: RNA Editing Enzyme and Methods of Use

TITLE OF INVENTION: Thereof

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howson and Howson

STREET: Spring House Corporate Cntr, P.O. Box 457

CITY: Spring House

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/280,443

FILING DATE: 17-FEB-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/197,794

FILING DATE: 17-FEB-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/280,443

FILING DATE: 25-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.

REGISTRATION NUMBER: 31,215

REFERENCE/DOCKET NUMBER: WST49AUSA

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-540-9206

TELEFAX: 215-540-5818

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 6671 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: unknown

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 155..3832

US-08-457-459-1

Query Match 72.4%; Score 15.2; DB 1; Length 6671;

Best Local Similarity 85.0%; Pred. No. 98;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TTGCTGAGACCGCTGCTGTC 21

Db 808 TTGCTATGACCGCTGCTGTC 789

RESULT 11

US-08-457-459-1/c

Sequence 1, Application US/08457459

Patent No. 5677428

GENERAL INFORMATION:

APPLICANT: Nishikura, Kazuko

TITLE OF INVENTION: RNA Editing Enzyme and Methods of Use

TITLE OF INVENTION: Thereof

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howson and Howson

STREET: Spring House Corporate Cntr, P.O. Box 457

CITY: Spring House

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/457,459

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/197,794

FILING DATE: 17-FEB-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/280,443

FILING DATE: 25-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.

REGISTRATION NUMBER: 31,215

REFERENCE/DOCKET NUMBER: WST49CUSA

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-540-9206

TELEFAX: 215-540-5818

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 6671 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: unknown

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 155..3832

US-08-457-459-1

Query Match 72.4%; Score 15.2; DB 1; Length 6671;

Best Local Similarity 85.0%; Pred. No. 98;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTGCTGTAGACCGTCTGGTC 21
DB 808 TTGGCTATGACCGTCTGGTC 789

RESULT 12
US-08-555-678-1/c
; Sequence 1, Application US/08555678
; Patent No. 5763174
; GENERAL INFORMATION:
; APPLICANT: Nishikura, Kazuko
; TITLE OF INVENTION: RNA Editing Enzyme and Methods
; TITLE OF INVENTION: of Use Thereof
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, P.O. Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,678
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,794
; FILING DATE: 17-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/280,443
; FILING DATE: 25-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/457,459
; FILING DATE: 01-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST49DUSA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9206
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6671 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 155..3832
; US-08-555-678-1

Query Match 72.4%; Score 15.2; DB 1; Length 6671;
Best Local Similarity 85.0%; Pred.No.98;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTGCTGTAGACCGTCTGGTC 21
DB 808 TTGGCTATGACCGTCTGGTC 789

RESULT 13
PCT-US95-02275-1/c
; Sequence 1, Application PC/TUS9502275
; GENERAL INFORMATION:
; APPLICANT: Wislar Institute of Anatomy & Biology
; ADDRESS: Wislar Institute of Anatomy & Biology
; STREET: Wislar Institute of Anatomy & Biology
; CITY: Wislar Institute of Anatomy & Biology
; STATE: Wislar Institute of Anatomy & Biology
; COUNTRY: Wislar Institute of Anatomy & Biology
; ZIP: Wislar Institute of Anatomy & Biology
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,678
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,794
; FILING DATE: 17-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/280,443
; FILING DATE: 25-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/457,459
; FILING DATE: 01-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST49DUSA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9206
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6671 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 155..3832
; US-08-555-678-1

; OTHER INFORMATION: /evidence= EXPERIMENTAL
US-08-419-448-31

Query Match 72.4%; Score 15.2; DB 2; Length 6756;
Best Local Similarity 85.0%; Pred. No. 98;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 TTGTCTGAGACCGTCTGTC 21
||| ||||| ||||| |||||
Db 130 TTATGAGACCGTCCGTC 149

Search completed: January 21, 2004, 13:11:48;
Job time : 63 secs

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 10:07:51 : Search time 799.5 Seconds
(without alignments)
1074.549 Million cell updates/sec

Title: US-09-913-325-5
Perfect score: 21
Sequence: 1 attgtctgagaccgtctggtc 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues 5777422

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_ov.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: gb_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_ov.*
22: em_ph.*
23: em_pat.*
24: em_pl.*
25: em_ro.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pin.*
35: em_htg_rdt.*
36: em_htg_mam.*
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41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

Result No.	Score	Query Match	Length	DB ID	Description
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2	21	100.0	396	6	AX093197 Sequence
3	21	100.0	482	6	BD117323 EST and e
4	21	100.0	491	6	BD027496 Sequence
5	21	100.0	512	6	BD071299 Sequence
6	21	100.0	1589	6	AX600212 Sequence
7	21	100.0	1648	6	AR208704 Sequence
8	21	100.0	1648	9	HUMTRPM2A
9	21	100.0	1651	6	A21577 blood plasm
10	21	100.0	1651	6	AR208714 Sequence
11	21	100.0	1651	9	HUMCLI
12	21	100.0	1658	9	BC019588 Homo sapi
13	21	100.0	1676	9	HSCSP40
14	21	100.0	1678	6	AX202086 Sequence
15	21	100.0	1684	9	BC010514 Homo sapi
16	21	100.0	1712	6	AX600209 Sequence
17	21	100.0	7610	6	AR208713 Sequence
18	21	100.0	7610	9	HUMTRPM2A1
19	21	100.0	134514	2	AC025192 Homo sapi
20	21	100.0	175475	9	AF235104 Homo sapi
21	21	100.0	234431	9	AF311103 Homo sapi
22	21	100.0	334051	2	AC123374 Rattus no
23	20	95.2	1545	9	AK093399 Homo sapi
24	19.4	92.4	181	6	AK093789 Sequence
25	19.4	92.4	221	6	AX701616 Sequence
26	17.8	84.8	66565	9	AC092103 Homo sapi
27	17.8	84.8	136131	9	AC000360 Homo sapi
28	17.8	84.8	147750	10	AC122503 Mus muscu
29	17.8	84.8	173513	9	HSJ125H2
30	17.8	84.8	180230	10	AC124692 Mus muscu
31	17.8	84.8	191410	10	AC083814 Mus muscu
32	17.8	84.8	227330	10	AC020786 Mus muscu
33	17.8	84.8	288888	9	HSJ10932 Homo sapi
34	17.4	82.9	177102	9	HSJ1069C8 Human DNA
35	17.4	82.9	225376	2	AC094230 Rattus no
36	17.4	82.9	225229	2	AC102656 Mus muscu
37	17.4	82.9	241215	2	AC113683 Rattus no
38	17.4	82.9	246769	2	AC094144 Rattus no
39	17.4	82.9	262108	2	AC105555 Rattus no
40	16.8	80.0	345	9	AY062323 Homo sapi
41	16.8	80.0	1785	6	AX653539 Sequence
42	16.8	80.0	10029	1	AE011998 Xanthomon
43	16.8	80.0	60786	2	AC124317 Homo sapi
44	16.8	80.0	120873	9	AL445986 Human DNA
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ALIGNMENTS

RESULT 1 AR302784/c AR302784 195 bp mRNA linear PAT 12-JUN-2003

LOCUS Sequence 14 from patent US 6541603.

DEFINITION AR302784

ACCESSION AR302784

VERSION AR302784.1 GI:31691271

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 195)

AUTHORS Kirschling,D.J., Gudkov,A. and Roninson,I.B.

TITLE Genes and genetic elements associated with sensitivity to platinum-based drugs

JOURNAL Patent: US 6541603-A 14 01-APR-2003;

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FEATURES
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Qy 1 ATTGCTGAGACCGCTCTGGTC 21
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Db 153 ATTGCTGAGACCGCTCTGGTC 133

RESULT 2
AX093197/c
LOCUS
DEFINITION Sequence 15 from Patent WO0118046.
ACCESSION AX093197
VERSION AX093197.1 GI:13509646
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  Xu, J. and Stolk, J. A.
  Ovarian tumor sequences and methods of use therefor
  Patent: WO 0118046-A 15 15-MAR-2001;
  CORIXA CORPORATION (US)
FEATURES
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      /db_xref="taxon:9606"
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  129 a 83 c 121 g 62 t 1 others
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  Best Local Similarity 100.0%; Pred. No. 3.2;
  Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATTGCTGAGACCGCTCTGGTC 21
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Db 145 ATTGCTGAGACCGCTCTGGTC 125

RESULT 3
BD117323/c
LOCUS
DEFINITION EST and encoded human protein.
ACCESSION BD117323
VERSION BD117323.1 GI:23212227
KEYWORDS JP 2002010789-A/9400.
SOURCE Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (Bases 1 to 482)
  Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.
  EST and encoded human protein
  Patent: JP 2002010789-A 9400 15-JAN-2002;
  GENSET CORP
COMMENT
  OS Homo sapiens (human)
  PN JP 2002010789-A/9400
  PD 15-JAN-2002
  PF 07-AUG-2000 JP 2000280989
  PR 05-AUG-1999 US 60/147499
  PI JEAN BAPTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EYE PI
  GIORDANO

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PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC
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  Best Local Similarity 100.0%; Pred. No. 3.1;
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Qy 1 ATTGCTGAGACCGCTCTGGTC 21
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Db 163 ATTGCTGAGACCGCTCTGGTC 143

RESULT 4
BD027496/c
LOCUS
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD027496
VERSION BD027496.1 GI:22569238
KEYWORDS JP 2001269182-A/3742.
SOURCE Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (Bases 1 to 491)
  Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
  Sequence tag and encoded human protein
  Patent: JP 2001269182-A 3742 02-OCT-2001;
  GENSET
COMMENT
  OS Homo sapiens (human)
  PN JP 2001269182-A/3742
  PD 02-OCT-2001
  PF 24-FEB-2000 JP 2000118773
  PR 26-FEB-1999 US 60/122487
  PI JEAN BAPTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
  JORDAN
  PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
  C12N5/10,
  PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
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CC score 6.3
CC seq LLPVGLLTWESG/QV
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BASE COUNT
  149 a 114 c 149 g 78 t 1 others
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  Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATTGCTGAGACCGCTCTGGTC 21
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Db 194 ATTGCTGAGACCGCTCTGGTC 174

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RESULT 5
BD071299/c
LOCUS BD071299 512 bp DNA linear PAT 27-AUG-2002
DEFINITION Secreted expressed sequence tags (sESTs).
ACCESSION BD071299
VERSION BD071299.1 GI:22616902
KEYWORDS JP 2001519667-A/109.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 512)
AUTHORS Jacobs,K., McCoy,J.M., Lavallie,E.R., Racie,L.A., Merberg,D., Tracy,M., Spaulding,V. and Agostino,M.J.
TITLE Secreted expressed sequence tags (sESTs)
JOURNAL Patent: JP 2001519667-A 109-23-OCT-2001;
COMMENT GENETICS INSTITUTE INC
OS Unidentified
PN JP 2001519667-A/109
PD 23-OCT-2001
PF 10-APR-1998 JP 1998543069
PI 10-APR-1997 US 08/838821
PI KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A RACIE, PI
DAVID MERBERG
PI MAURICE TREACY,VIKKI SPAULDING,MICHAEL J AGOSTINO PC
C12N15/12,C12N5/10,C07K14/47,C12Q1/68,A61K38/17 CC Strandedness:
Double;
CC Topology: Linear;
CC Secreted expressed sequence tags (sESTs)
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FT /organism='Unidentified'.
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Query Match 100.0%; Score 21; DB 6; Length 512;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATTGCTGAGACCGTCTGGTC 21
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Db 121 ATTGCTGAGACCGTCTGGTC 101
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RESULT 6
AX600212/c
LOCUS AX600212 1589 bp DNA linear PAT 14-FEB-2003
DEFINITION Sequence 24 from Patent WO02072830.
ACCESSION AX600212
VERSION AX600212.1 GI:28400254
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Yue,H., Yao,M.G., Ison,C.H., Lu,Y., Warren,B.A., Elliott,V.S., Baughn,M.R., Ding,L., Xu,Y., Gietzen,K.J., Tang,T.Y., Lai,P.G., Duggan,B.M., Burford,N., Lu,D.A., Richardson,T.W., Tran,U.K., Khare,R. and Walla,N.K.
TITLE Proteins associated with cell growth, differentiation, and death
JOURNAL Patent: WO 02072830-A 24 19-SEP-2002;
COMMENT Incyte Genomics, Inc. (US)
FEATURES
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Location/Qualifiers
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
/note='Incyte ID No: 7503618CB1'
BASE COUNT 407 a 421 c 466 g 295 t
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Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATTGCTGAGACCGTCTGGTC 21
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Db 164 ATTGCTGAGACCGTCTGGTC 144
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RESULT 7
AR208704/c
LOCUS AR208704 1648 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 3 from patent US 6383808.
ACCESSION AR208704
VERSION AR208704.1 GI:21509928
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1648)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 3 07-MAY-2002;
FEATURES
source
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Location/Qualifiers
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BASE COUNT 408 a 488 c 440 g 312 t
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Db 139 ATTGCTGAGACCGTCTGGTC 119
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RESULT 8
HUMTRPM2A/c
LOCUS HUMTRPM2A 1648 bp mRNA linear PRI 23-AUG-1996
DEFINITION Human TRPM-2 mRNA, complete cds.
ACCESSION M64722
VERSION M64722.1 GI:339972
KEYWORDS TRPM-2 protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (sites), Pineault,J., Lakins,J., Taillefer,D., Leger,J., Wang,C. and Tenniswood,M.
JOURNAL Genomic organization and expression of the rat TRPM-2 (clusterin) gene, a gene implicated in apoptosis
MEDLINE J. Biol. Chem. 268 (7), 5021-5031 (1993)
PUBMED 93186813
PUBMED 7650346
REFERENCE 2 (bases 1 to 1648)
AUTHORS Wong,P., Taillefer,D., Lakins,J., Pineault,J., Chader,G. and Tenniswood,M.
TITLE Molecular characterization of human TRPM-2/clusterin, a gene associated with sperm maturation, apoptosis and neurodegeneration
JOURNAL Eur. J. Biochem. 221 (3), 917-925 (1994)
MEDLINE 94237156
PUBMED 8181474
COMMENT source text: Human cDNA to mRNA.
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Location/Qualifiers
/organism='Homo sapiens'

/translation="MKTKLLFVGLLLTWESGVLDGDTVSDNELOEMSGNOGSKYVKNK
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LLENDROTHMLDVMQDFSRASSIIDELEFQDRFTRPDQTYHYLPSLPHRRPHE
FPKSRIVSLMPFSPPELNFHMFQPFLEHQAQADIHHSFAPQHPPTFFIRE
GDDRTVCREIRHNSGCKRILSDCTNNPSQAKIRELDSQVAE
RLTRKYNELLSYQWMLNTGSLLEQLNEQFNWVSRLANLTQGEDDYLRVTTVASH
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199..261
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262..876
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877..1542
/product="complement cytolysis inhibitor b-chain"
BASE COUNT 405 a 481 c 447 g 318 t
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Query Match 100.0%; Score 21; DB 9; Length 1651;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATTGCTGAGACCGTCTGGTC 21
Db 282 ATTGCTGAGACCGTCTGGTC 262
BC019588 1658 bp mRNA linear PRI 17-APR-2003
Homo sapiens clusterin (complement lysis inhibitor, SP-40, 40,
sulphated glycoprotein 2, testosterone-repressed prostate message 2,
apolipoprotein J), mRNA (CDNA clone MGC:24903 IMAGE:4915444),
complete cds.
BC019588
BC019588.1 GI:18043614
MGC.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1658)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zesberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,I., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullaby,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.O. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
JOURNAL 2388257
MEDLINE 12477932
PUBMED 2 (bases 1 to 1658)
REFERENCE Strausberg,R.
AUTHORS Direct Submission
TITLE Submitted (19-DEC-2001) National Institutes of Health, Mammalian
JOURNAL Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk

Email: cgabs-i@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louised, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 29 Row: m Column: 21
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4502904.
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sulphated glycoprotein 2, testosterone-repressed prostate
message 2, apolipoprotein J)"
/protein_id="AAH19588.1"
/db_xref="GI:18043615"
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EIONAVNGVQIKTLIEKTEBERKTLISLEAKKKEDALNETRESSTKIKELPGVC
NETMALWRECEPKLCKOTCKFYARVCRSGSLVGLQLEFLNQSPPFYFWMGDRID
SLENDROTHMLDVMQDFSRASSIIDELEFQDRFTRPDQTYHYLPSLPHRRPHE
FPKSRIVSLMPFSPPELNFHMFQPFLEHQAQADIHHSFAPQHPPTFFIRE
EGDDRTVCREIRHNSGCKRILSDCTNNPSQAKIRELDSQVAE
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Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATTGCTGAGACCGTCTGGTC 21
Db 135 ATTGCTGAGACCGTCTGGTC 115
RESULT 13
HSCSP40/C
LOCUS HSCSP40 1676 bp mRNA linear PRI 22-MAR-1995
DEFINITION Human SP-40, 40 mRNA for complement-associated protein SP-40, 40
alpha-1 and beta-1 chain.
X14723
ACCESSION X14723.1 GI:30250
VERSION
KEYWORDS complement-associated protein; serum protein; SP-40, 40 gene.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1676)

Kirsbaum, L., Sharpe, J.A., Murphy, B., d'Apice, A.J., Classon, B., Hudson, P. and Walker, I.D.

Molecular cloning and characterization of the novel, human complement-associated protein, SP-40,40: a link between the complement and reproductive systems

EMBO J. 8 (3), 711-718 (1989)

89251601

2721499

2 (bases 1 to 1676)

Kirsbaum, L.

Direct Submission

Submitted (17-MAR-1989) Kirsbaum L., The University of Melbourne, The Preclinical Centre, School of Veterinary Science, Parkville Victoria 3052, Australia

The sequence overlaps with that reported by Murphy et. al. in J. Clin. Invest. 81:1858-1864(1988).

Location/Qualifiers

1..1676

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="LK (107)"

/tissue_type="liver"

/clone_lib="lambda gt11"

48..1397

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/codon_start=1

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/db_xref="GI:30251"

/db_xref="SWISS-PROT:P10909"

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48..113

/note="signal peptide (AA -22 to -1)"

729..1394

/product="mature alpha-chain (AA 205-427)"

114..1394

/note="SP-40,40 propetide (AA 1-427)"

114..5114

/note="beta-chain"

1622..1627

/note="pot. polyA signal"

BASE COUNT 436 a 488 c 437 g 315 t

ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 1676;

Best Local Similarity 100.0%; Pred. No. 2.9;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGCTGGTC 21

Db 134 ATTGCTGAGACCGCTGGTC 114

RESULT 14

AX202086/c

LOCUS

DEFINITION Sequence 16 from Patent WO0153511.

ACCESSION AX202086

VERSION AX202086.1 GI:15391872

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 Phippard, D., Vasanthakamur, G., Dotson, S. and Ma, X.J.

Osteoarthritis tissue derived nucleic acids, polypeptides, vectors, and cells

Patent: WO 0153531-A 16.26-JUL-2001;

Pharmacia Corporation (US)

Location/Qualifiers

1..1678

/organism="Homo sapiens"

/mol_type="genomic DNA"

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BASE COUNT 424 a 491 c 450 g 313 t

ORIGIN

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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGCTGGTC 21

Db 156 ATTGCTGAGACCGCTGGTC 136

RESULT 15

BC010514/c

LOCUS

DEFINITION Homo sapiens clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein U), mRNA (cDNA clone MGC:18080 IMAGE:4150452), complete cds.

ACCESSION BC010514

VERSION BC010514.1 GI:14714740

KEYWORDS MGC.

SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1684)

STRAUSBERG, R.L., FEINGOLD, E.A., GROUSE, L.H., DERGE, J.G., KLAUSNER, R.D., COLLINS, F.S., WAGNER, L., SHENMEN, C.M., SCHULER, G.D., ALTSCHUL, S.F., ZEEBERG, B., BUETOW, K.H., SCHAEFER, C.F., BHAT, N.K., HOPKINS, R.F., JORDAN, H., MOORE, T., MAX, S.I., WANG, J., HSIEH, F., DIATCHENKO, L., MARIUSIN, K., FARMER, A.A., RUBIN, G.M., HONG, L., STAPLETON, M., SOARES, M.B., BONALDO, M.F., CASAVANT, T.L., SCHEETZ, T.E., BROWNSTEIN, M.J., USIDIN, T.B., TOSHIYUKI, S., CARNINCI, P., PRANGE, C., RAHA, S.S., LOQUELLANO, N.A., PETERS, G.J., ABRAMSON, R.D., MULLAHDY, S.J., BOSAK, S.A., MCEWAN, P.J.J., MCKERNAN, K.J., MALEK, J.A., GUNARATNE, P.H., RICHARDS, S., WORLEY, K.C., HALE, S., GARCIA, A.M., GAY, L.J., HULYK, S.W., VILLALON, D.K., MUZNY, D.M., SODERGREN, E.J., LU, X., GIBBS, R.A., FAHEY, J., HELTON, E., KETTEMAN, M., MADAN, A., YOUNG, A.C., SHAYCHENKO, Y., SANCHEZ, A., WHITING, M., TOUCHMAN, J.W., GREEN, E.D., BOUFFARD, G.G., BLAKESLEY, R.W., TOUCHMAN, J.W., GREEN, E.D., DICKSON, M.C., RODRIGUEZ, A.C., GRIMWOOD, J., SCHMUTZ, J., MYERS, R.M., BUTTERFIELD, Y.S., KRZYWINSKI, M.I., SKALSKA, U., SMALLIS, D.E., SCHNERCH, A., SCHEIN, J.E., JONES, S.J. and MARRA, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 1684)

STRAUSBERG, R.

Direct Submission

Submitted (10-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabbs-remail.nih.gov

Tissue Procurement: David N. Louis, M.D.

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: the I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: angbcm.tmc.edu
Gunnarathne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 19 Row: 0 Column: 12.

FEATURES

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69..1418

gene

CDS

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sulfated glycoprotein 2, testosterone-repressed prostate
message 2, apolipoprotein J)"
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SLLENDROTHMDVMQDHFSPASSIIDELFQDRFETREPQDTHYLPSPHRRPHF
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BASE COUNT

433 a 493 c 448 g 310 t

ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 1684;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTCTCTGACCGCTCTGTC 21

Db 155 ATGTCTGACCGCTCTGTC 135

Search completed: January 21, 2004, 12:11:43
Job time : 807 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 10:59:47 ; Search time 1733 seconds

(without alignments)
294.515 Million cell updates/sec

Title: US-09-913-325-5

Perfect score: 21

Sequence: 1 attgtctgagaccgtctggtc 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_estc:*

9: gb_est1:*

10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_est6:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_man:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_pbg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	152	9 AW161759	AW161759 au70a10.x
2	21	100.0	156	10 BF922862	BF922862 QV4-NT024
3	21	100.0	161	10 BF921576	BF921576 MR1-NT017
4	21	100.0	165	10 BF929381	BF929381 IL2-NT019

C	5	21	100.0	167	10 BF929953	BF929953 IL2-NT019
C	6	21	100.0	169	10 BE766895	BE766895 RC2-NT011
C	7	21	100.0	177	9 AL048592	AL048592 DRF2P586H
C	8	21	100.0	177	10 BF958041	BF958041 RC5-NN116
C	9	21	100.0	184	10 BF958930	BF958930 PM1-NN120
C	10	21	100.0	185	12 EI036860	EI036860 MR4-NT014
C	11	21	100.0	190	12 EI037432	EI037432 CM3-NT026
C	12	21	100.0	193	10 BF944445	BF944445 RC5-NN116
C	13	21	100.0	196	9 AI745406	AI745406 WC37D01.X
C	14	21	100.0	201	10 BF957666	BF957666 PM1-NN120
C	15	21	100.0	207	10 BF957858	BF957858 PM1-NN120
C	16	21	100.0	207	10 AW807875	AW807875 MR4-STC09
C	17	21	100.0	218	9 AI904991	AI904991 IL-BT072-
C	18	21	100.0	220	10 BF920102	BF920102 MR1-NT017
C	19	21	100.0	223	10 BF920102	AW161224 au70a10.y
C	20	21	100.0	224	9 AW161224	BF935119 MR4-NT014
C	21	21	100.0	226	10 BF935119	BE841947 MR4-STC09
C	22	21	100.0	227	10 BE841947	BF950916 CM3-NN021
C	23	21	100.0	229	10 BF950916	AA333299 EST44448
C	24	21	100.0	236	9 AA332929	BF921875 CM3-NT017
C	25	21	100.0	238	10 BF921875	BF923639 MR4-NT014
C	26	21	100.0	243	9 AA336628	AA336628 EST41242
C	27	21	100.0	244	10 BE766870	BE766870 RC2-NT011
C	28	21	100.0	248	10 BF923643	BF923643 MR4-NT014
C	29	21	100.0	252	10 BF923633	BF923633 MR4-NT014
C	30	21	100.0	253	10 BF87875	BF87875 OV2-TN017
C	31	21	100.0	253	12 EI041998	EI041998 MR4-NT014
C	32	21	100.0	256	12 EI041248	EI041248 MR4-NT014
C	33	21	100.0	257	9 AA365743	AA365743 EST76594
C	34	21	100.0	262	10 BF947155	BF947155 MR3-NN021
C	35	21	100.0	262	13 BQ339859	BQ339859 PM1-NN120
C	36	21	100.0	266	9 AA352030	AA352030 EST59959
C	37	21	100.0	268	10 BF920149	BF920149 MR1-NT017
C	38	21	100.0	272	10 BF956582	BF956582 PM1-NN120
C	39	21	100.0	273	10 BF956584	BF956584 PM1-NN120
C	40	21	100.0	274	12 EI036852	EI036852 MR4-NT014
C	41	21	100.0	277	9 AA351754	AA351754 EST59817
C	42	21	100.0	280	10 BF935974	BF935974 IL2-NT019
C	43	21	100.0	283	10 BF947214	BF947214 MR3-NN021
C	44	21	100.0	284	12 EG995096	EG995096 CMO-HT129
C	45	21	100.0	293	9 AA318247	AA318247 EST20305

ALIGNMENTS

RESULT 1

AW161759

LOCUS

DEFINITION

IMAGE:2781594 3' similar to gb:XI4723 CLUSTERIN PRECURSOR (HUMAN);

mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AW161759 152 bp mRNA linear EST 09-NOV-1999
au70a10.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone
IMAGE:2781594 3' similar to gb:XI4723 CLUSTERIN PRECURSOR (HUMAN);
mRNA sequence.

AW161759 GI:6300792

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 152)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,

Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin

, J., Moore, B., Scheilenberg, K., Steptoe, M., Tan, F., Theising, B.,

White, Y., Wylie, T., Waterston, R. and Wilson, R.

WashU-NCI human EST Project

Unpublished

Other ESTs: au70a10.y1

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco.

FEATURES

Location/Qualifiers
1. .152

source

/organism="Homo sapiens"
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/lab_host="DH10B"
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/note="Organ: brain; Vector: pBluescript SK (Stratagene); Site 1: SstI; Site 2: XhoI; Double-stranded cDNA was prepared from human fetal brain tissue. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence:
5'-GAGAGAGAGAGAGCTCAAGATCCTTAATAATTAATCCCCCCCCC-3' and 3' adaptor sequence:
5'-GAGAGAGAGAGCTCGAGTTTCTTTTCTTTT-3'. The library was size-selected for >0.5 kb inserts and has an average insert size estimated at 1.2 kb. This library was constructed using the CAP-trapper method for full-length enrichment and has not undergone amplification. Library was constructed by Dr. Claudio Schneider (LNCIB-Area Science Park, Trieste, Italy)."

BASE COUNT

27 a

43 c

28 g

54 t

Query Match 100.0%; Score 21; DB 9; Length 152;

Best Local Similarity 100.0%; Pred. NO. 7.1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATTGCTGAGACCGCTCGTC 21

Db 100 ATTGCTGAGACCGCTCGTC 120

RESULT 2

BF922862/c

LOCUS

BF922862 QV4-NT0247-201100-262-g12 NT0247 Homo sapiens cDNA, mRNA sequence. EST 19-JAN-2001

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

CONTACT

LABORATORY

INSTITUTE

FOR RESEARCH

ADDRESS

TELEPHONE

FAX

EMAIL

PROJECT

URL

THIS ENTRY CAN BE SEEN IN THE FOLLOWING URL

PROJECT. THIS ENTRY CAN BE SEEN IN THE FOLLOWING URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV4&t2=QV4-NT0247-201100-262-g12&t3=2000-11-20&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 15

High quality sequence stop: 155.

FEATURES

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/note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT

38 a

30 c

51 g

37 t

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Best Local Similarity 100.0%; Pred. No. 7.2;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 94 ATTGCTGAGACCGCTCGTC 74

RESULT 3

BF921576/c

LOCUS

BF921576 MRI-NT0179-171100-004-g01 NT0179 Homo sapiens cDNA, mRNA sequence. EST 19-JAN-2001

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

CONTACT

LABORATORY

INSTITUTE

FOR RESEARCH

ADDRESS

TELEPHONE

FAX

EMAIL

PROJECT

URL

THIS ENTRY CAN BE SEEN IN THE FOLLOWING URL

PROJECT. THIS ENTRY CAN BE SEEN IN THE FOLLOWING URL

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Site 2: SmaI; A mini-library was made by cloning products
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No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
44 a 29 c 53 g 35 t

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Best Local Similarity 100.0%; Pred. No. 7.3; Indels 0; Gaps 0;
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QY 1 ATTGCTGAGACCGCTCGTC 21
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DB 101 ATTGCTGAGACCGCTCGTC 81

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BF929381
LOCUS IL2-NT0198-081200-280-G01 NT0198 Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION BF929381
VERSION BF929381.1 GI:12327509
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 165)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-NT0198-
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Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

FEATURES
source
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-NT0198-
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High quality sequence stop: 165.
Location/Qualifiers
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Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 44 a 29 c 53 g 35 t
ORIGIN
Query Match 100.0%; Score 21; DB 10; Length 161;
Best Local Similarity 100.0%; Pred. No. 7.3; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

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DB 101 ATTGCTGAGACCGCTCGTC 81

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LOCUS IL2-NT0198-111200-293-A03_1 NT0198 Homo sapiens cDNA, mRNA
DEFINITION
ACCESSION BF929953
VERSION BF929953.1 GI:12328185
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 167)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-NT0198-
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Seq primer: puc 18 forward
High quality sequence stop: 165.
Location/Qualifiers
1..167
/organism="Homo sapiens"
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/dev_stage="Adult"
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/notes="Organ: nervous tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 60 a 32 c 48 g 27 t
ORIGIN
Query Match 100.0%; Score 21; DB 10; Length 167;
Best Local Similarity 100.0%; Pred. No. 7.4; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

QY 1 ATTGCTGAGACCGCTCGTC 21
|||||

```


COMMENT
Contact: Simpson A.J.G.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-NN1165-
281100-033-E03&t3=2000-11-28&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 177.

FEATURES
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NN1165"
/note="Organ: nervous normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
47 a 34 c 52 g 28 t

BASE COUNT
63 a 34 c 52 g 28 t

ORIGIN
Query Match 100.0%; Score 21; DB 10; Length 177;
Best Local Similarity 100.0%; Pred. No. 7.5; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTCGAGACCGTCGTGTC 21
|||||
Db 68 ATTGCTCGAGACCGTCGTGTC 48
|||||

RESULT 9
BF958930/c
LOCUS
BF958930 184 bp mRNA linear EST 22-JAN-2001
DEFINITION
PM1-NN1200-011200-009-g08 NN1200 Homo sapiens cDNA, mRNA sequence.
ACCESSION
BF958930.1 GI:12376205
VERSION
EST.
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 184)
AUTHORS
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL
MEDLINE
20202663
PUBMED
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-NN1165-
281100-033-E03&t3=2000-11-28&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 177.

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/clone_lib="NN1200"
/note="Organ: nervous normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
47 a 36 c 61 g 40 t

BASE COUNT
47 a 36 c 61 g 40 t

ORIGIN
Query Match 100.0%; Score 21; DB 10; Length 184;
Best Local Similarity 100.0%; Pred. No. 7.6; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTCGAGACCGTCGTGTC 21
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Db 108 ATTGCTCGAGACCGTCGTGTC 88
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RESULT 10
BI036860/c
LOCUS
BI036860 185 bp mRNA linear EST 14-JUN-2001
DEFINITION
MR4-NT0140-080101-209-c09 NT0140 Homo sapiens cDNA, mRNA sequence.
ACCESSION
BI036860
VERSION
BI036860.1 GI:14443486
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 185)
AUTHORS
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL
MEDLINE
20202663
PUBMED
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
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Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&t2=MR4-NT0140-
080101-209-c09&t3=2001-01-08&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 134.
High quality sequence stop: 134.

FEATURES
source
1..185
Location/Qualifiers
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/mol_type="mRNA"

/db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="NT0140"
 /note="Organ: nervous tumor; Vector: puc18; Site: 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 low stringency conditions." 40 t

BASE COUNT

41 a 42 c 62 g 40 t

ORIGIN

Query Match 100.0%; Score 21; DB 12; Length 185;
 Best Local Similarity 100.0%; Pred. No. 7.6;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGTCTGGTC 21
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 Db 109 ATTGCTGAGACCGTCTGGTC 89

RESULT 11

BI037432 190 bp mRNA linear EST 14-JUN-2001
 LOCUS CM3-NT0267-110101-588-h12 NT0267 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BI037432
 ACCESSION BI037432
 VERSION BI037432.1 GI:14444058
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 190)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

10737800

CONTACT: Simpson A.J.G.

Laboratory of Cancer Genetics

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 Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-NT0267-
 110101-588-h12&t3=2001-01-11&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 4

High quality sequence stop: 190.

Location/Qualifiers

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/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="NT0267"

/note="Organ: nervous tumor; Vector: puc18; Site: 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under

BASE COUNT 76 a 38 c 49 g 27 t

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 7.7;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGTCTGGTC 21
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 Db 36 ATTGCTGAGACCGTCTGGTC 16

RESULT 12

BF944445/c

LOCUS

DEFINITION

ACCESSION

BF944445

VERSION

BF944445.1 GI:12361720

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 193)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

10737800

CONTACT: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

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 Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-NN1165-
 131000-021-D04&t3=2000-10-13&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 193.

Location/Qualifiers

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/organism="Homo sapiens"

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/clone_lib="NN1165"

/note="Organ: nervous normal; Vector: puc18; Site 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 low stringency conditions." 27 t

BASE COUNT 70 a 39 c 57 g 27 t

ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 193;
 Best Local Similarity 100.0%; Pred. No. 7.8;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGTCTGGTC 21
 |||||

Db	72	ATTGCTGAGACCGTCTGGTC	52	
RESULT 13				
AI745406				
LOCUS	196 bp	mrna	linear	EST 17-DEC-1999
DEFINITION	wc37d01.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:2320801 3' similar to gb:X14723 CLUSTERIN PRECURSOR (HUMAN);, mRNA sequence.			
ACCESSION	AI745406	1	GI:5113694	
VERSION	EST.			
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM				
REFERENCE				
AUTHORS	1	(bases 1 to 196)		
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap . National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index			
JOURNAL	Unpublished			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-re@mail.nih.gov Tissue procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Insert Length: 264 Std Error: 0.00 Seq primer: -40UP from Gibco.			
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source	1..196			
	/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:2320801" /sex="male" /dev_stage="adult" /lab_host="DH103" /clone_lib="NCI-CGAP Pr28" /note="Organ: Prostate; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP Pr22 was prepared, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Donaldo."			
BASE COUNT	39 a	60 c	35 g	62 t
ORIGIN				
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Best Local Similarity	100.0%;	Pred. No. 7.8;		
Matches	21;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
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Db	101	ATTGCTGAGACCGTCTGGTC	121	
RESULT 14				
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LOCUS	201 bp	mrna	linear	EST 22-JAN-2001
DEFINITION	PM1-NN1200-251100-007-c09 NN1200 Homo sapiens cDNA, mRNA sequence.			
ACCESSION	BF957666	1	GI:12374941	
VERSION	EST.			
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM				
REFERENCE				
AUTHORS	1	(bases 1 to 207)		
TITLE	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
JOURNAL				
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM1&t2=PM1-NN1200-251100-007-c09&t3=2000-11-25&t4=1) Seq primer: puc 18 forward High quality sequence start: 14 High quality sequence stop: 201. Location/Qualifiers 1..201 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /dev_stage="Adult" /clone_lib="NN1200" /note="Organ: nervous normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."			
BASE COUNT	52 a	39 c	71 g	39 t
ORIGIN				
Query Match	100.0%;	Score 21;	DB 10;	Length 201;
Best Local Similarity	100.0%;	Pred. No. 7.9;		
Matches	21;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	ATTGCTGAGACCGTCTGGTC	21	
Db	125	ATTGCTGAGACCGTCTGGTC	105	
RESULT 15				
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LOCUS	207 bp	mrna	linear	EST 22-JAN-2001
DEFINITION	PM1-NN1200-271100-008-a07 NN1200 Homo sapiens cDNA, mRNA sequence.			
ACCESSION	BF957858	1	GI:12375133	
VERSION	EST.			
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM				
REFERENCE				
AUTHORS	1	(bases 1 to 207)		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
JOURNAL				
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM1&t2=PM1-NN1200-251100-007-c09&t3=2000-11-25&t4=1) Seq primer: puc 18 forward High quality sequence start: 14 High quality sequence stop: 201. Location/Qualifiers 1..201 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /dev_stage="Adult" /clone_lib="NN1200" /note="Organ: nervous normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."			
BASE COUNT	52 a	39 c	71 g	39 t
ORIGIN				

sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202653
 PUBMED 10737800
 COMMENT
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM1&t2=PM1-NN1200-271100-008-a07&t3=2000-11-27&t4=1>)
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 High quality sequence start: 24
 High quality sequence stop: 182.
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 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 BASE COUNT 51 a 45 c 71 g 40 t
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 Query Match 100.0%; Score 21; DB 10; Length 207;
 Best Local Similarity 100.0%; Pred. No. 8;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATTGCTGAGACCGCTGCTC 21
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 Db 143 ATTGCTGAGACCGCTGCTC 123

Search completed: January 21, 2004, 13:09:41
 Job time : 1738 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 10:04:17 ; Search time 148 Seconds
(without alignments)
383.028 Million cell updates/sec

Title: US-09-913-325-5

Perfect score: 21
Sequence: 1 attgtctgagaccgtctggtc 21

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2522756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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25: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	21	AAA94227 Human testosterone
2	21	100.0	195	16	AAT00416 Genetic suppressor
3	21	100.0	396	22	AAF94824 Human ovarian carc
4	21	100.0	396	24	ABT03091 Human ovarian carc
5	21	100.0	396	24	ABL48774 Ovarian carcinoma
6	21	100.0	491	21	AAC03751 Human secreted pro
7	21	100.0	512	20	AAV89150 EST clone CGI, Ho
8	21	100.0	572	20	AAZ42136 Human normal bladd

ALIGNMENTS

RESULT 1

AAA94227

ID AAA94227 standard; DNA; 21 BP.

XX AAA94227;

XX 12-JAN-2001 (first entry)

XX Human testosterone-repressed prostate message-2 antisense oligo #3.

XX Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;
XX sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.

XX Homo sapiens.

XX WO200049937-A2.

XX 31-AUG-2000.

XX 25-FEB-2000; 2000WO-US04875.

XX 26-FEB-1999; 99US-0121726.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX Gleave M, Rennie PS, Miyake H, Nelson C;
XX WPI; 2000-533132/48.

XX Treating prostatic tumors and renal cancers by antisense inhibition of
XX the testosterone-repressed prostate messenger-2 gene -

Human ovarian anti
Human secreted exp
Toxicologically re
cDNA encoding nove
Human cDNA encodin
Human clusterin ge
Cytolysis inhibito
Human clusterin ge
Osteoarthritis tis
Human cDNA encodin
Human clusterin ge
Human G protein-co
Human secreted pro
Human secreted pro
Human secreted pro
Human secreted pro
Human secreted pro
Human structural p
Arabidopsis thalia
cDNA encoding nove
Human Oestrogen re
Bifidobacterium lo
Bifidobacterium lo
Human immune/haema
Human colon cancer
DNA encoding novel
Human reproductive
Nucleotide sequenc
EP-892047 Seq ID 4
DNA encoding CARDI
Drosophila melanog
Drosophila melanog
Drosophila melanog
Drosophila melanog
Drosophila melanog
Human cDNA differe
Human DNA containi

XX Claim 4; Page 36; 38pp; English.

XX The present sequence is an antisense oligonucleotide directed at the

XX human testosterone-repressed prostate message-2 (TRPM-2), also known as

XX clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to

XX promote the regression of tumours, and oligonucleotides directed

XX at human TRPM-2 can be used in the treatment of tumour cells expressing

XX the TRPM-2 gene. These include prostate cancer, renal cell cancer and

XX some breast cancer cells. In addition to this, they also increase the

XX chemosensitivity of the cells, meaning that conventional chemotherapy is

XX more effective.

XX SQ Sequence 21 BP; 3 A; 5 C; 6 G; 7 T; 0 other;

Query Match 100.0%; Score 21; DB 21; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.25; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATTGCTGAGACCGCTGTGGTC 21

Db 1 ATTGCTGAGACCGCTGTGGTC 21

RESULT 2

AAT00416/c

ID AAT00416 standard; cDNA; 195 BP.

XX AC AAT00416;

XX DT 26-MAR-1996 (first entry)

XX DE Genetic suppressor element HU7.1.

XX KW Genetic suppressor element; GSE; platinum-based drug; cisplatin;

XX KW chemotherapy; HU7.1; testosterone-repressed prostatic message-2; TRPM-2;

XX KW ss.

XX OS Synthetic.

XX PN WO9522612-A2.

XX PD 24-AUG-1995.

XX PF 22-FEB-1995; 95WO-US02303.

XX PR 22-FEB-1994; 94US-0199900.

XX PA (UNII) UNIV ILLINOIS FOUND.

XX PI Gudkov A, Kirschling DJ, Robinson IB;

XX DR WPI; 1995-302718/39.

XX Genetic suppressor elements which confer resistance to

XX platinum-based drugs, eg. cisplatin, on cancer cells - useful for

XX enhancement of chemotherapy, and for diagnosis of resistance to

XX these drugs.

XX Claim 14; Fig 17; 75pp; English.

XX The sequences represented by AAT00405-T00418 are genetic suppressor

XX elements (GSEs). This sequence represents GSE HL6.10. This sequence

XX shows homology to the cDNA encoding testosterone-repressed prostatic

XX message-2 (TRPM-2). These sequences were obtained from a cDNA library

XX derived from the total cDNA of a cisplatin sensitive cell. Genetic

XX suppressor elements confer resistance to platinum-based drugs (PDs),

XX such as cisplatin. These functional GSEs can then be used to create

XX probes for the parent gene. The probes can then be used in a method of

XX measuring the level of GSE gene expression. The GSEs can be used in

XX methods of diagnosis of resistance to PDs by measuring the level of

XX expression of GSE genes. The GSEs are also used in methods to overcome

XX resistance to PDs in cancer cells. The GSEs (or fragments of them) can

CC be used to inhibit the function of genes associated with sensitivity to

CC PDs. For enhancement of chemotherapy, a GSE can be transferred (either

CC alone or with another gene) on an expression vector into blood to

CC progenitor cells from a cancer patient. The cells are returned to the

CC patients circulation and allowed to repopulate the blood before

CC aggressive chemotherapy is carried out (using higher cisplatin

CC concentrations than normal), this will thereby avoid toxic side effects

CC to the immune system as the blood cells will be GSE resistant.

XX SQ Sequence 195 BP; 46 A; 45 C; 71 G; 33 T; 0 other;

Query Match 100.0%; Score 21; DB 16; Length 195;

Best Local Similarity 100.0%; Pred. No. 0.37;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATTGCTGAGACCGCTGTGGTC 21

Db 153 ATTGCTGAGACCGCTGTGGTC 133

RESULT 3

AAF94824/c

ID AAF94824 standard; cDNA; 396 BP.

XX AC AAF94824;

XX DT 23-MAY-2001 (first entry)

XX DE Human ovarian cancer associated coding sequence SEQ ID NO: 15.

XX KW Human, ovarian cancer; vaccine; gene therapy; carcinoma; ss.

XX OS Homo sapiens.

XX PN WO200118046-A2.

XX PD 15-MAR-2001.

XX PF 08-SEP-2000; 2000WO-US24827.

XX PR 10-SEP-1999; 99US-0394374.

XX PR 01-MAY-2000; 2000US-0561778.

XX PR 15-AUG-2000; 2000US-0640173.

XX PR 07-SEP-2000; 2000US-0656668.

XX PA (CORI-) CORIXA CORP.

XX PI Xu J, Stolk JA;

XX DR WPI; 2001-211395/21.

XX Isolated polypeptides associated with ovarian carcinomas, and the

XX nucleic acids that encode them, useful for the prevention diagnosis and

XX treatment of ovarian cancers -

XX Claim 18; Page 120; 189pp; English.

XX The present invention provides a number of coding sequences and proteins,

XX the over-expression of which is associated with ovarian carcinoma/cancer.

XX These can be used in the diagnosis, treatment and prevention of ovarian

XX cancer, optionally by gene therapy or in the form of a vaccine. The

XX present sequence is an example of one of these sequences.

XX SQ Sequence 396 BP; 129 A; 83 C; 121 G; 62 T; 1 other;

Query Match 100.0%; Score 21; DB 22; Length 396;

Best Local Similarity 100.0%; Pred. No. 0.42;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATTGCTGAGACCGCTGTGGTC 21

Db 145 ATTGCTGAGACCGCTGTGGTC 125

RESULT 4
 ABL48774/c
 ID ABL48774 standard; cDNA; 396 BP.
 XX AC ABL48774;
 XX DT 05-SEP-2002 (first entry)
 XX DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 15.
 XX KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
 XX KW cytosolic; gene; ss.
 XX OS Homo sapiens.
 XX PN WO200239885-A2.
 XX PD 23-MAY-2002.
 XX PF 13-NOV-2001; 2001WO-US45395.
 XX PR 14-NOV-2000; 2000US-0713550.
 XX PR 03-APR-2001; 2001US-0825294.
 XX PR 02-OCT-2001; 2001US-0970966.
 XX PA (CORI-) CORIXA CORP.
 XX PI Xu J, Stolk JA, Algate PA, Fling SP, Molesch DA;
 XX WPI; 2002-500186/53.
 XX The novel ovarian cancer polypeptide and polynucleotide, useful for
 PT detecting the presence of ovarian cancer in a patient, and in
 PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
 PT -
 XX Example 1; Page 117; 197pp; English.
 XX The present invention provides human ovarian cancer associated proteins
 CC and coding sequences. The sequences can be used in the diagnosis and
 CC treatment of ovarian cancers. The present sequence is a coding sequence
 CC of the invention.
 XX SQ Sequence 396 BP; 129 A; 83 C; 121 G; 62 T; 1 other;
 Query Match 100.0%; Score 21; DB 24; Length 396;
 Best Local Similarity 100.0%; Pred. No. 0.42; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATTGCTGAGACCGCTGCTGTC 21
 Db 145 ATTGCTGAGACCGCTGCTGTC 125

RESULT 5
 ABL48774/c
 ID ABL48774 standard; cDNA; 396 BP.
 XX AC ABL48774;
 XX DT 18-JUN-2002 (first entry)
 XX DE Ovarian carcinoma sequence isolate 23657.1.
 XX KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
 XX KW ss.
 XX OS Homo sapiens.
 XX PN US2002004491-A1.
 XX PD 10-JAN-2002.

XX PF 03-APR-2001; 2001US-0825294.
 XX PR 10-SEP-1999; 99US-0394374.
 XX PR 01-MAY-2000; 2000US-0561778.
 XX PR 15-AUG-2000; 2000US-0640173.
 XX PR 07-SEP-2000; 2000US-0656668.
 XX PR 14-NOV-2000; 2000US-0713550.
 XX (XUJ/) XU J.
 XX (STOL/) STOLK J A.
 XX (ALGA/) ALGATE P A.
 XX (FLIN/) FLING S P.
 XX Xu J, Stolk JA, Algate PA, Fling SP;
 XX WPI; 2002-171027/22.
 XX Ovarian tumour polypeptide and polynucleotide useful in diagnosis, -
 PT prevention and/or treatment of cancer, especially ovarian cancer
 XX Example 1; Page 43; 131pp; English.
 XX The invention relates to ovarian tumour polynucleotides and polypeptides
 CC that may be utilised in cancer therapy, for example in a vaccine or
 CC gene therapy. Polypeptides and polynucleotides of the invention are
 CC useful for detecting a cancer in a patient, for stimulating and/or
 CC expanding T-cells specific for a tumour protein, and for inhibiting the
 CC development of a cancer in a patient. They are also useful for
 CC stimulating an immune response in a patient and for treating a cancer in
 CC a patient and for determining the presence of a cancer in a patient.
 CC The isolated polynucleotides of the invention are useful for their
 CC ability to selectively form duplex molecules with complementary stretches
 CC of the entire desired gene or gene fragments, and for designing and
 CC preparing ribozyme molecules for inhibiting expression of tumour
 CC polypeptides in tumour cells. Polypeptides and polynucleotides of the
 CC invention are also useful in recombinant DNA molecules to direct
 CC expression of a polypeptide in appropriate host cells. The sequences
 CC given in records ABL48760-ABL48956 represent polynucleotides encoding
 CC ovarian carcinoma proteins.
 XX SQ Sequence 396 BP; 129 A; 83 C; 121 G; 62 T; 1 other;
 Query Match 100.0%; Score 21; DB 24; Length 396;
 Best Local Similarity 100.0%; Pred. No. 0.42; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATTGCTGAGACCGCTGCTGTC 21
 Db 145 ATTGCTGAGACCGCTGCTGTC 125

RESULT 6
 AAC03751/c
 ID AAC03751 standard; cDNA; 491 BP.
 XX AC AAC03751;
 XX DT 06-OCT-2000 (first entry)
 XX DE Human secreted protein 5' EST, SEQ ID NO: 3749.
 XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 XX KW gene therapy; chromosome mapping; ss.
 XX OS Homo sapiens.
 XX PN EP1033401-A2.
 XX PD 06-SEP-2000.
 XX PF 21-FEB-2000; 2000EP-0200610.
 XX

PR 26-FEB-1999; 99US-0122487.
 XX (GBST) GENSET.
 XX Dumas Milne Edwards J, Duclert A, Giordano J;
 XX WPI; 2000-500381/45.
 DR P-PSDB; AAG03745.
 XX
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX
 XX Claim 1; SEQ ID 3749; 71pp + CD-ROM; English.
 XX
 CC The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. An ORF has been identified within the
 CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
 CC derived from 30 different tissues. EST sequences usually correspond
 CC mainly to the 3' untranslated region (UTR) of the mRNA because they are
 CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
 CC well suited for isolating cDNA sequences derived from the 5' ends of
 CC mRNAs and even in those cases where longer cDNA sequences have been
 CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
 CC mRNAs with intact 5' ends and can therefore be used to obtain full length
 CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
 CC gene therapy and chromosome mapping procedures. They are used to obtain
 CC upstream regulatory sequences and to design expression and secretion
 CC vectors.
 XX
 XX Sequence 491 BP; 149 A; 114 C; 149 G; 78 T; 1 other;
 SQ
 Query Match 100.0%; Score 21; DB 21; Length 491;
 Best Local Similarity 100.0%; Pred. No. 0.43;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATTGCTCTGAGACCGCTCTGGTC 21
 |||||
 DB 194 ATTGCTCTGAGACCGCTCTGGTC 174
 |||||
 RESULT 7
 AAV89150/c
 ID AAV89150 standard; cDNA; 512 BP.
 AC AAV89150;
 XX
 XX 15-FEB-1999 (first entry)
 DT
 XX EST clone CGL.
 DE
 XX Human; secreted protein; expressed sequence tag; EST; haematopoiesis;
 KW tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic;
 KW receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;
 KW gene therapy; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO9845436-A2.
 PN
 XX 15-OCT-1998.
 PD
 XX 10-APR-1998; 98WO-US06955.
 PF
 XX 10-APR-1997; 97US-0838821.
 PR
 XX (GEMY) GENETICS INST INC.
 PA
 XX Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
 PI Racie LA, Spaulding V, Treacy M;
 XX WPI; 1999-070077/06.
 DR
 XX

PT New polynucleotides encoding human secreted proteins - derived from
 PT e.g. human blood, kidney, foetal lung, placenta, testes, brain,
 PT ovary, pituitary, retina and colon cDNA libraries.
 XX
 XX Claim 1; Page 126; 618pp; English.
 XX
 CC The present sequence represents a human expressed sequence tag (EST).
 CC The polynucleotide, which is a secreted EST, and the encoded protein
 CC are predicted to have useful biological activities which would make
 CC them suitable for treating, preventing or ameliorating medical
 CC conditions in humans and animals, although no supporting data is
 CC given. Suggested activities include nutritional activity, immune
 CC stimulating or suppressing activity, haematopoiesis regulating
 CC activity, tissue growth activity, activin/inhibin activity,
 CC chemotactic/chemokinetic activity, haemostatic and thrombolytic
 CC activity, receptor/ligand activity, anti-inflammatory activity,
 CC cadherin/tumour invasion suppressor activity, tumour inhibition
 CC activity. The polynucleotide may also be useful for gene therapy.
 XX
 XX Sequence 512 BP; 154 A; 114 C; 150 G; 94 T; 0 other;
 SQ
 Query Match 100.0%; Score 21; DB 20; Length 512;
 Best Local Similarity 100.0%; Pred. No. 0.43;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATTGCTCTGAGACCGCTCTGGTC 21
 |||||
 DB 121 ATTGCTCTGAGACCGCTCTGGTC 101
 |||||
 RESULT 8
 AAZ42136/c
 ID AAZ42136 standard; cDNA; 572 BP.
 XX
 XX AAZ42136;
 AC
 XX 31-JAN-2000 (first entry)
 DT
 XX Human normal bladder tissue cDNA derived EST 15.
 DE
 XX Human; bladder; treatment; EST; expressed sequence tag; cytostatic;
 KW cancer; gene therapy; ss.
 KW
 XX Homo sapiens.
 OS
 XX DE19818620-A1.
 PN
 XX 28-OCT-1999.
 PD
 XX 21-APR-1998; 98DE-1018620.
 PF
 XX 21-APR-1998; 98DE-1018620.
 PR
 XX (META-) METAGEN GES GENOMFORSCHUNG MBH.
 PA
 XX Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
 PI WPI; 1999-602416/52.
 DR
 XX New polypeptides and their nucleic acids, useful for treatment of
 PT bladder tumour and identification of therapeutic agents -
 PT
 XX Claim 3; Page 158; 366pp; German.
 XX
 CC This invention describes novel polypeptide fragment sequences (I) and
 CC their encoding nucleic acids (II) which are highly expressed in normal
 CC bladder tissue and have cytostatic activity. (II) are used for
 CC recombinant expression of (I) and to isolate complete genes. (I) are
 CC used to identify agents suitable for the treatment of bladder tumours,
 CC to directly treat this form of cancer (including expression from gene
 CC therapy vectors), or are used in a preparation for cancer treatment. (I)
 CC is also used for the generation of specific antibodies. (II) are
 CC identified by assembling ESTs (expressed sequence tags) from a

particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, and therefore reduces the number of failures because of ESTs from different libraries representing different parts of the same unknown gene. CC
 CC distorting the estimated frequency of occurrence in a particular tissue. CC
 CC AA24122-24248 represent EST fragments derived from a human normal CC
 CC bladder tissue cDNA library which encode the protein fragments CC
 CC represented in AAY60329-Y60591. CC
 CC
 CC Sequence 572 BP; 161 A; 128 C; 186 G; 97 T; 0 other; CC
 CC
 CC Query Match 100.0%; Score 21; DB 20; Length 572; CC
 CC Best Local Similarity 100.0%; Pred. No. 0.44; 0; Indels 0; Gaps 0; CC
 CC Matches 21; Conservative 0; Mismatches 0; CC
 CC
 CC QY 1 ATTGCTGAGACCGTCTGGTC 21 CC
 CC ||||| CC
 CC Db 262 ATTGCTGAGACCGTCTGGTC 242 CC
 CC
 CC RESULT 9 CC
 CC ABQ56105/c CC
 CC ID ABQ56105 standard; cDNA; 704 BP. CC
 CC AC ABQ56105; CC
 CC XX 22-AUG-2002 (first entry) CC
 CC XX
 CC DE Human ovarian antigen HSPSH41 cDNA, SEQ ID NO:1985. CC
 CC XX
 CC KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; CC
 CC KW ovarian cancer; breast cancer; tumour; reproductive system disorder; CC
 CC KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; CC
 CC KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; CC
 CC KW inflammatory condition; immune disorder; blood disorder; CC
 CC KW cardiovascular disorder; respiratory disorder; neurological disorder; CC
 CC KW gastrointestinal disorder; urinary system disorder; drug screening; CC
 CC KW gene therapy; chromosome mapping; forensic analysis; CC
 CC KW antibody preparation; cytostatic; immunomodulatory; neuroprotective; CC
 CC KW antiinflammatory; gynaecological; reproductive; gene; ss. CC
 CC XX
 CC OS Homo sapiens. CC
 CC XX
 CC PN WO200200677-A1. CC
 CC XX
 CC PD 03-JAN-2002. CC
 CC XX
 CC XX 07-JUN-2001; 2001WO-US18569. CC
 CC PF
 CC XX 07-JUN-2000; 2000US-209467P. CC
 CC PR
 CC XX (HUMA-) HUMAN GENOME SCI INC. CC
 CC PA
 CC XX Birse CE, Rosen CA; CC
 CC XX
 CC DR WPI; 2002-147878/19. CC
 CC DR P-PSDB; ABP43028. CC
 CC XX
 CC PT Isolated nucleic acid molecules encoding novel ovarian polypeptides, CC
 CC PT useful in the prevention treatment and diagnosis of cancer (e.g. CC
 CC PT ovarian cancer), immune disorders, cardiovascular disorders and CC
 CC PT neurological diseases - CC
 CC XX
 CC PS Claim 1; SEQ ID NO 1985; 2922pp; English. CC
 CC XX
 CC CC The invention relates to 2175 novel human ovarian antigens (ABP41054- CC
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also CC
 CC CC encompasses polypeptides 90% identical and polynucleotides 95% identical CC
 CC CC to the sequences of the invention. The invention additionally relates to CC
 CC CC recombinant vectors and host cells comprising human ovarian antigen CC
 CC CC polynucleotides, antibodies against human ovarian antigens, and the use CC
 CC CC of ovarian antigen polynucleotides and polypeptides in diagnosing, CC
 CC CC treating, prognosing or preventing various ovary and/or breast-related

disorders. Such conditions include ovarian cancer and breast cancer, and CC
 CC metastatic tumours of ovarian or breast origin, reproductive system CC
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation, CC
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine CC
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic CC
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and CC
 CC vaginitis), immune disorders (e.g., congenital and acquired CC
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), CC
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders, CC
 CC respiratory disorders, neurological disorders, gastrointestinal disorders CC
 CC and urinary system disorders. Ovarian antigen polypeptides and CC
 CC polynucleotides may also be used in screening for compounds which CC
 CC modulate ovarian antigen expression or activity. The polynucleotides may CC
 CC further be used for gene therapy, chromosome mapping, in the CC
 CC identification of individuals and in forensic analysis, and the CC
 CC polypeptides may be used as food additives or to prepare antibodies CC
 CC useful in disease diagnosis, drug targeting and phenotyping. The present CC
 CC sequence represents cDNA encoding a human ovarian antigen of the CC
 CC invention. CC
 CC Note: The sequence data for this patent did not form part of the printed CC
 CC specification, but was obtained in electronic format directly from WIPO CC
 CC at ftp.wipo.int/pub/published_pct_sequences. CC

Sequence 704 BP; 180 A; 197 C; 199 G; 121 T; 7 other; CC
 CC
 CC Query Match 100.0%; Score 21; DB 24; Length 704; CC
 CC Best Local Similarity 100.0%; Pred. No. 0.46; CC
 CC Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0; CC

QY 1 ATTGCTGAGACCGTCTGGTC 21 CC
 CC ||||| CC
 CC Db 215 ATTGCTGAGACCGTCTGGTC 195 CC

RESULT 10 CC
 CC AAA43857/c CC
 CC ID AAA43857 standard; cDNA; 922 BP. CC

XX AAA43857; CC

XX 21-AUG-2000 (first entry) CC

XX Human secreted expressed sequence tag SEQ ID NO:432. CC

Human; mouse; chicken; rat; secreted expressed sequence tag; sEST; CC
 CC expressed sequence tag; EST; probe; chemotactic; proliferative; CC
 CC immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic; CC
 CC thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal; CC
 CC antiviral; antidiabetic; antiasthmatic; vulnery; antiparkinsonian; CC
 CC anticancer; osteoprotective; neuroprotective; nootropic; antipsoriatic; CC
 CC cerebroprotective; anticonvulsant; antidepressant; gene therapy; CC
 CC vaccine; autoimmune disorder; multiple sclerosis; allergic condition; CC
 CC insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer; CC
 CC lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; CC
 CC central nervous system disorder; Alzheimer's disease; stroke; CC
 CC Parkinson's disease; Huntington's disease; coagulation disorder; CC
 CC haemophilia; thrombosis; inflammatory disorder; Crohn's disease; CC
 CC tumour; infection; depression; psoriasis; ss. CC

XX Homo sapiens. CC

OS WO2000021991-A1. CC

XX 20-APR-2000. CC

XX 15-OCT-1999; 99WO-US24206. CC

XX 15-OCT-1998; 98US-0104436. CC

XX (GENY) GENETICS INST INC. CC

XX Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C; CC
 CC Merberg D, Treacy M, Bowman MR; CC

XX DR WPI; 2000-317938/27.

XX PT Isolated polynucleotides, and encoded proteins, comprising secreted

PT expressed sequence tags (ESTs), useful for treating various disorders

PT such as autoimmune, infectious, and central nervous system disorders -

XX

PS Claim 1; Page 316; 803pp; English.

XX CC AAA43426 to AAA45925 represent specifically claimed secreted expressed

CC sequence tags (ESTs), isolated from human, mouse, chicken and rat

CC tissue sources. The ESTs can have a range of activities depending on

CC the tissues they were isolated from. The activities include:

CC chemotactic; proliferative; immunomodulatory; haematopoietic;

CC chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory;

CC cyostatic; antibacterial; antifungal; antiviral; antidiabetic;

CC antiasthmatic; vulnerary; antitumor; osteopathic; neuroprotective;

CC neurotropic; antiparkinsonian; antipsoriatic; cerebroprotective;

CC anticonvulsant; and antidepressant. The ESTs can be used for gene

CC therapy and in vaccines. The ESTs are useful as probes for the

CC identification and isolation of full-length cDNAs and genomic DNA

CC molecules which correspond to the ESTs. Proteins encoded by the ESTs

CC are useful in assays for determining biological activity and raising

CC antibodies. They may be useful for treatment of autoimmune disorders

CC - (multiple sclerosis, insulin dependent diabetes), allergic conditions

CC (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,

CC osteoporosis, osteoarthritis, central nervous system disorders

CC (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation

CC disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's

CC disease), tumours, bacterial, fungal or viral infections, depression and

CC psoriasis. AAA45926 to AAA45931 represent linker variants which are given

CC in the exemplification of the present invention.

XX

SQ Sequence 922 BP; 243 A; 265 C; 244 G; 166 T; 4 other;

Query Match 100.0%; Score 21; DB 21; Length 922;

Best Local Similarity 100.0%; Pred. No. 0.48;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATTGCTCGAGACCGCTCTGGTC 21

Db 118 ATTGCTCGAGACCGCTCTGGTC 98

RESULT 11

ABZ83527/c

ID ABZ83527 standard; cDNA; 1024 BP.

XX AC ABZ83527;

XX DT 14-MAY-2003 (first entry)

XX DE Toxicologically relevant human nucleotide sequence #686.

XX KW Toxicologically relevant gene; toxicological response; gene; ss.

XX OS Homo sapiens.

XX PN W0203016500-A2.

XX PD 27-FEB-2003.

XX PF 16-AUG-2002; 2002WO-US26514.

XX PR 16-AUG-2001; 2001US-313080P.

XX PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.

XX PI Neft RE, Dunn RT, Adkins K, Pickett GG, Kier LD, Schweizer K;

XX PI Alien P;

XX DR WPI; 2003-268322/26.

XX

PT Determining a toxicological response to an agent, useful for screening

PT of drugs, comprises comparing the expression profile of one or more

PT human toxic response genes to a reference gene expression profile

PT indicative of toxicity -

XX Claim 1; Page 232; 455pp; English.

XX CC The present invention describes a method (M1) for determining a

CC toxicological response to an agent, which comprises comparing the

CC expression profile of one or more human toxic response genes to a

CC reference gene expression profile indicative of toxicity, and so

CC determining the presence of a toxic response to the agent. Also

CC described: (1) an array comprising one or more polynucleotides selected

CC from the genes corresponding to the partial sequences given in AB282842

CC to AB284764, or their fragments of at least 20 nucleotides, or

CC homologues; and (2) determining if a gene putatively identified to be a

CC toxic response gene plays a role on toxic response pathways by

CC determining the expression profile of the gene after exposure of cells

CC or a human subject to a known toxic pharmaceutical or industrial agent,

CC comprising: (a) exposing cells to an agent; (b) obtaining the test gene

CC expression profile for a putatively identified toxic response gene after

CC exposure to a known toxic pharmaceutical or industrial agent; and

CC (c) comparing the test profile to the expression profile of a gene with

CC a similar function or comparing the test profile to the expression

CC profile of that gene after exposure to other known toxic compounds. The

CC methods are useful for predicting and determining toxicological responses

CC on a cellular, organ or system level. The arrays comprising the human

CC genes are useful for toxicological screening of drugs, pharmaceutical

CC compounds and chemicals.

XX

SQ Sequence 1024 BP; 262 A; 299 C; 278 G; 185 T; 0 other;

Query Match 100.0%; Score 21; DB 25; Length 1024;

Best Local Similarity 100.0%; Pred. No. 0.49;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATTGCTCGAGACCGCTCTGGTC 21

Db 134 ATTGCTCGAGACCGCTCTGGTC 114

RESULT 12

AAS44948/c

ID AAS44948 standard; cDNA; 1568 BP.

XX AC AAS44948;

XX DT 18-DEC-2001 (first entry)

XX DE cDNA encoding novel human secretory protein, Seq ID No 29.

XX KW Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;

XX KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;

XX KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;

XX KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;

XX KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;

XX KW gut protection; lung; liver fibrosis; immune deficiency; infection;

XX KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;

XX KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;

XX KW fertility; analgesic; pain; antigen; ss.

XX OS Homo sapiens.

XX PN W0200166689-A2.

XX PD 13-SEP-2001.

XX PF 05-MAR-2001; 2001WO-US04942.

XX PR 07-MAR-2000; 2000US-0519705.

XX PR 19-MAY-2000; 2000US-0574454.

XX PR 17-JUN-2000; 2000US-0596193.

PR 14-JUL-2000; 2000US-0616847.
 PR 19-SEP-2000; 2000US-0665363.
 PR 20-OCT-2000; 2000US-0693267.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren P, Ma Y, Zhou P;
 PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AD, Wang J;
 FI WPI; 2001-589934/56.
 DR P-PSDB; AAU28048.
 XX Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis and treatment of
 PT cancer, neurological, inflammatory, and autoimmune disorders -
 XX
 XX Claim 1; SEQ ID No 29; 107pp; English.
 XX The invention relates to novel isolated human secreted polypeptides (I)
 CC and polynucleotides (II). (I) and (II) are useful for treating
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
 CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
 CC involved in increasing haematopoiesis, stem cell survival, bone growth
 CC and remodeling. (I), (II) and modulators of (II) are useful for
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for
 CC creating transgenic animals useful for studying the in vivo activities of
 CC the polypeptide as well as for studying modulators of the polypeptides.
 CC (I) induces the proliferation of neural cells and regeneration of nerve
 CC and brain tissue and is useful for the treatment of central and
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth, and in tissue repair, healing of burns, incisions,
 CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
 CC disorders, or periodontal disease. Furthermore, (I) is also useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, various immune deficiencies and
 CC disorders including severe combined immunodeficiency (SCID), bacterial or
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
 CC reactions and conditions, such as asthma or other respiratory problems.
 CC In addition, (I) affects biorhythms or circadian cycles of rhythms,
 CC fertility, metabolism, catabolism, anabolism, storage or elimination of
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
 CC analgesic effects or other pain reducing effects, immunoglobulin like
 CC activity and can act as an antigen in a vaccine composition to raise an
 CC immune response. AAS44920-AAS45295 represent novel human secreted protein
 CC coding sequences of the invention.
 XX
 XX Sequence 1568 BP; 386 A; 456 C; 434 G; 292 T; 0 other;
 SQ
 Query Match 100.0%; Score 21; DB 22; Length 1568;
 Best Local Similarity 100.0%; Pred. No. 0.52;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATTGCTGACACCGTCTGGTC 21
 Db 156 ATTGCTGACACCGTCTGGTC 136
 RESULT 13
 ABS78654/c
 ID ABS78654 standard; cDNA; 1589 BP.
 XX
 XX AC ABS78654;
 XX
 XX 16-DEC-2002 (first entry)
 DT
 XX Human cDNA encoding CGDD12, INCYTE 7503618CB1.
 DE
 XX

KW Human; ss; gene; cell growth; differentiation; death; CGDD; cancer;
 KW cell proliferative disorder; arteriosclerosis; atherosclerosis;
 KW cirrhosis; hepatitis; paroxysmal nocturnal haemoglobinuria; psoriasis;
 KW polycythaemia vera; primary thrombocytopaenia; developmental disorder;
 KW renal tubular acidosis; anaemia; mental retardation; epilepsy; AIDS;
 KW neurological disorder; Alzheimer disease; Parkinson's disease; asthma;
 KW reproductive disorder; infertility; autoimmune disorder; gout; allergy;
 KW inflammatory disorder; acquired immunodeficiency syndrome; uveitis;
 KW autoimmune thyroiditis; contact dermatitis; Crohn's disease; infection;
 KW diabetes mellitus; glomerulonephritis; irritable bowel syndrome;
 KW multiple sclerosis; osteoarthritis; osteoporosis; pancreatitis;
 KW rheumatoid arthritis.
 XX Homo sapiens.
 OS
 XX WO200272830-A2.
 PN
 XX 19-SEP-2002.
 PD
 XX 08-FEB-2002; 2002WO-US03715.
 XX
 XX 09-FEB-2001; 2001US-268111P.
 XX 23-FEB-2001; 2001US-271175P.
 PR
 XX 08-MAR-2001; 2001US-274503P.
 PR
 XX 09-MAR-2001; 2001US-274552P.
 PR
 XX (INCY-) INCYTE GENOMICS INC.
 PA
 XX Yue H, Yao MG, Ison CH, Lu Y, Warren BA, Elliott VS, Baughn MR;
 PI Ding L, Xu Y, Gietzen KJ, Tang TY, Lal PG, Duggan BM, Burford N;
 PI Lu DAM, Richardson TW, Tran UK, Khare R, Walla NK;
 XX WPI; 2002-723356/78.
 DR P-PSDB; ABG97361.
 XX
 XX New human proteins associated with cell growth, differentiation and
 PT death, useful for diagnosing, treating or preventing autoimmune or
 PT inflammatory disorders (e.g. AIDS, allergy or anemia), cancer,
 PT atherosclerosis or hepatitis -
 XX
 XX Claim 5; Page 180-181; 181pp; English.
 PS
 XX The invention relates to an isolated polypeptide comprising CGDD1-12
 CC (cell growth, differentiation and death), a naturally occurring amino
 CC acid sequence at least 90% identical to CGDD, a biologically active
 CC fragment or an immunogenic fragment. Also included are the
 CC polynucleotides encoding CGDD1-12, a recombinant polynucleotide
 CC comprising a promoter sequence operably linked to the CGDD
 CC polynucleotides, a cell transformed with the recombinant polynucleotide,
 CC a transgenic organism comprising the recombinant polynucleotide, an
 CC anti-CGDD antibody, screening for compounds which bind to/modulate
 CC or are ant/agonists of CGDD or alter the expression of CGDD
 CC polynucleotide and a CGDD polynucleotide microarray.
 CC The polypeptides, polynucleotides, agonists and antagonists are
 CC useful for diagnosing, treating or preventing disorders associated with
 CC aberrant expression of CGDD, particularly cell proliferative (e.g.
 CC arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal
 CC nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary
 CC thrombocytopaenia or cancer), developmental disorders (e.g. renal
 CC tubular acidosis, anaemia or mental retardation), neurological disorders
 CC (e.g. Alzheimer disease, Parkinson's disease or epilepsy),
 CC reproductive disorders (e.g. infertility or a disruption in the
 CC menstrual cycle), or autoimmune/inflammatory disorders (e.g. AIDS,
 CC acquired immunodeficiency syndrome) allergies, asthma, autoimmune
 CC thyroiditis, contact dermatitis, Crohn's disease, diabetes mellitus,
 CC glomerulonephritis, gout, irritable bowel syndrome, multiple sclerosis,
 CC osteoarthritis, osteoporosis, pancreatitis, rheumatoid arthritis,
 CC uveitis, or viral, bacterial, fungal, parasitic, protozoal or helminthic
 CC infections. They are also useful in the assessment of the effects of
 CC exogenous compounds on the expression of nucleic acid and amino acid
 CC sequences of proteins associated with CGDD. The present sequence
 CC encodes a CGDD protein.
 CC
 XX

SQ Sequence 1589 BP; 407 A; 421 C; 466 G; 295 T; 0 other;
 Query Match 100.0%; Score 21; DB 24; Length 1589;
 Best Local Similarity 100.0%; Pred. No. 0.53;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGCTCTGGTC 21
 |||||
 DB 164 ATTGCTGAGACCGCTCTGGTC 144

RESULT 14
 ABN99656/c
 ID ABN99656 standard; DNA; 1648 BP.
 XX
 AC ABN99656;
 XX
 DT 16-AUG-2002 (first entry)
 XX
 DE Human clusterin gene sequence 1.
 XX
 KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
 KW hypercholesterolaemia; cardiovascular disorder; ds;
 KW hyperproliferative disorder; hyperlipidemic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200222635-A1.
 XX
 PD 21-MAR-2002.
 XX
 PF 10-SEP-2001; 2001WO-US28235.
 XX
 PR 11-SEP-2000; 2000US-0659791.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Prefer SM;
 XX
 DR WPI; 2002-404805/43.
 DR P-PSDB; AAO15039.
 XX
 PT Novel antisense compound targeted to nucleic acid molecule encoding
 PT clusterin, useful for treating animal having disease associated with
 PT clusterin such as hyperlipidemic disorder, cardiovascular disorder -
 XX
 PS Example 13; Page 89-92; 125pp; English.
 XX
 CC The invention comprises antisense oligonucleotides that are capable of
 CC inhibiting expression of the human clusterin gene. The antisense
 CC oligonucleotides of the invention are useful for inhibiting the
 CC expression of clusterin in cells. The antisense oligonucleotides are also
 CC useful for treating an animal with a disease or condition associated with
 CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
 CC hyperproliferative disorders; and hyperlipidemic disorders). The present
 CC DNA sequence represents a human clusterin gene sequence.
 XX
 SQ Sequence 1648 BP; 408 A; 488 C; 440 G; 312 T; 0 other;
 Query Match 100.0%; Score 21; DB 24; Length 1648;
 Best Local Similarity 100.0%; Pred. No. 0.53;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGCTCTGGTC 21
 |||||
 DB 139 ATTGCTGAGACCGCTCTGGTC 119

RESULT 15
 AAO11503/c
 ID AAO11503 standard; DNA; 1651 BP.
 XX
 AC AAO11503;

XX 20-JUN-1991 (first entry)
 DT Cytolysis Inhibitor gene.
 DE Cytolysis inhibitor; perforin; immunological effector molecule;
 KW infertility; ss.
 KW Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT sig_peptide 199..261
 FT /*tag= a
 FT mat_peptide 262..1542
 FT /*tag= b
 FT /product= cytolysis inhibitor
 XX
 PN DE3933850-A.
 XX
 PD 18-APR-1991.
 XX
 PF 06-OCT-1989; 89DE-3933850.
 XX
 PR 06-OCT-1989; 89DE-3933850.
 XX
 PA (SCHD) SCHERING AG.
 XX
 PI Tschopp J, Jenne D;
 XX
 DR WPI; 1991-118338/17.
 XX
 PT DNA sequence coding for cytolysis inhibitor - is strong inhibitor
 PT of terminal complement protein, e.g. perforin secreted by killer
 PT cells
 XX
 PS Claim 2; Page 8; 15pp; German.
 XX
 CC Two probes were prepared based on the known partial amino acid
 CC sequences of both chains of the Cytolysis Inhibitor and used to
 CC screen a liver-specific cDNA library. One clone which hybridised
 CC positively to both probes was found to contain a 1.7kb BamHI-XbaI
 CC fragment. This was inserted into plasmid pGEM4, to give pGEM4/ZI-1.
 CC E.coli transformed with the plasmid are deposited under DSM # 5269.
 CC The insert has the sequence given in this file.
 CC See also AAO11501 and AAO11502.
 XX
 SQ Sequence 1651 BP; 405 A; 481 C; 447 G; 318 T; 0 other;
 Query Match 100.0%; Score 21; DB 12; Length 1651;
 Best Local Similarity 100.0%; Pred. No. 0.53;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGCTCTGGTC 21
 |||||
 DB 282 ATTGCTGAGACCGCTCTGGTC 262

Search completed: January 21, 2004, 11:44:45
 Job time : 151 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 12:11:53 ; Search time 217 Seconds
(without alignments)

341.106 Million cell updates/sec

Title: US-09-913-325-5
Perfect score: 21
Sequence: 1 attgtctgagaccgtctgtgc 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2324096 seqs, 1762381658 residues

Total number of hits satisfying chosen parameters: 4649192

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
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3: /cgn2_6/prodata/2/pubpna/US05_NEW_PUB.seq:
4: /cgn2_6/prodata/2/pubpna/US06_PUBCOMB.seq:
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11: /cgn2_6/prodata/2/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:
14: /cgn2_6/prodata/2/pubpna/US10A_PUBCOMB.seq:
15: /cgn2_6/prodata/2/pubpna/US10B_PUBCOMB.seq:
16: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:
17: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq:
18: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	10	US-09-944-326-5
2	21	100.0	21	13	Sequence 5, Appli
3	21	100.0	21	13	Sequence 5, Appli
	21	100.0	21	13	Sequence 5, Appli
C 4	21	100.0	195	12	US-10-404-579-14
C 5	21	100.0	396	9	US-09-825-294-15
C 6	21	100.0	396	10	US-09-970-965-15
C 7	21	100.0	396	12	US-10-369-186-15
C 8	21	100.0	396	13	US-10-361-811-15
C 9	21	100.0	396	16	US-10-212-677-15
C 10	21	100.0	461	11	US-09-918-995-32172
C 11	21	100.0	462	11	US-09-918-995-2524
C 12	21	100.0	465	11	US-09-918-995-32177
C 13	21	100.0	492	11	US-09-918-995-31156
C 14	21	100.0	532	10	US-09-833-381-910
C 15	21	100.0	539	11	US-09-918-995-31688

C 16	21	100.0	704	12	US-10-364-049-1985
C 17	21	100.0	1451	13	US-10-133-013-214
C 18	21	100.0	1568	12	US-10-291-172-29
C 19	21	100.0	1614	13	US-10-119-428-31
C 20	21	100.0	1678	10	US-09-765-231A-16
C 21	21	100.0	1775	13	US-10-133-013-243
C 22	21	100.0	2090	13	US-09-814-353-20893
C 23	19.4	92.4	181	12	US-10-404-579-19
C 24	19.4	92.4	490	11	US-09-918-995-12511
C 25	19.4	92.4	491	11	US-09-918-995-17455
C 26	18.4	87.6	277	10	US-09-833-381-1241
C 27	17.8	84.8	1670	11	US-09-832-129-11
C 28	17.8	84.8	1684	11	US-09-832-129-11
C 29	17.4	82.9	516	11	US-09-918-995-31131
C 30	16.8	80.0	387	15	US-10-156-761-7326
C 31	16.8	80.0	9025608	15	US-10-156-761-1
C 32	16.2	77.1	1728	10	US-09-938-842A-1616
C 33	16.2	77.1	2304	12	US-10-291-172-405
C 34	16.2	77.1	2462	12	US-10-104-047-255
C 35	15.8	75.2	355	15	US-10-106-698-1758
C 36	15.8	75.2	559	13	US-10-029-386-1057
C 37	15.8	75.2	755	15	US-10-013-315-47
C 38	15.8	75.2	1228	11	US-09-919-039-24
C 39	15.8	75.2	1580	11	US-09-764-891-9304
C 40	15.8	75.2	2652	12	US-10-104-047-807
C 41	15.8	75.2	8888	9	US-09-836-077-41
C 42	15.8	75.2	43412	12	US-10-085-117-7
C 43	15.4	73.3	374	12	US-10-428-681-53
C 44	15.2	72.4	25	15	US-10-098-263B-102072
C 45	15.2	72.4	332	11	US-09-764-891-1943

ALIGNMENTS

RESULT 1

US-09-944-326-5
; Sequence 5, Application US/09944326
; Patent No. US20020128220A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY
; FILE REFERENCE: UBC P-020-2
; CURRENT APPLICATION NUMBER: US/09/944,326
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 5
; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-09-944-326-5

Query Match 100.0%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGCTGTGTC 21

DB 1 ATTGCTGAGACCGCTGTGTC 21

RESULT 2

US-09-967-726A-5

```
Sequence 5, Application US/09967726A
; Publication No. US20030159130A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Zellweger, Tobias
; TITLE OF INVENTION: Chemo- and Radiation-Sensitization of Cancer by Antisense TRPM-2
; FILE REFERENCE: UBC.P-022
; CURRENT APPLICATION NUMBER: US/09/967,726A
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-09-967-726A-5

Query Match 100.0%; Score 21; DB 13; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATTGCTGAGACCGCTCGTC 21
Db 1 ATTGCTGAGACCGCTCGTC 21

RESULT 3
US-10-080-794-5
; Sequence 5, Application US/10080794
; Publication No. US20030166591A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY USING AN OLIGONUCLEOTIDE
; FILE REFERENCE: UBC.P-020-3
; CURRENT APPLICATION NUMBER: US/10/080,794
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 09/944,326
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-10-080-794-5

Query Match 100.0%; Score 21; DB 13; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATTGCTGAGACCGCTCGTC 21
Db 1 ATTGCTGAGACCGCTCGTC 21

RESULT 4
US-10-404-579-14/c
; Sequence 14, Application US/10404579
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Publication No. US20040002099A1
; GENERAL INFORMATION:
; APPLICANT: Kirschling, Deborah J
; APPLICANT: Gudkov, Andrei
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; with Sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/404,579
; FILING DATE: 01-Apr-2003
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,657A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20040002099A1nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-404-579-14

Query Match 100.0%; Score 21; DB 12; Length 195;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATTGCTGAGACCGCTCGTC 21
Db 153 ATTGCTGAGACCGCTCGTC 133

RESULT 5
US-09-825-294-15/c
; Sequence 15, Application US/09825294
; Patent No. US20020004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 396
; TYPE: DNA
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-15

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Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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   |||||
Db 145 ATTGCTGAGACCGTCTGGTC 125

RESULT 6
US-09-970-966-15/c
; Sequence 15, Application US/09970966
; Patent No. US2002017363A1
; GENERAL INFORMATION:
; APPLICANT: Moleah, David Alan
; APPLICANT: Stolk, John A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C6
; CURRENT APPLICATION NUMBER: US/09/970,966
; CURRENT FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 333
; OTHER INFORMATION: n = A,T,C or G
US-09-970-966-15

Query Match      100.0%; Score 21; DB 10; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGTCTGGTC 21
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Db 145 ATTGCTGAGACCGTCTGGTC 125

RESULT 7
US-10-369-186-15/c
; Sequence 15, Application US/10369186
; Publication No. US20030232056A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C9
; CURRENT APPLICATION NUMBER: US/10/369,186
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 333
; OTHER INFORMATION: n = A,T,C or G
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US-10-369-186-15

Query Match      100.0%; Score 21; DB 12; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGTCTGGTC 21
   |||||
Db 145 ATTGCTGAGACCGTCTGGTC 125

RESULT 8
US-10-361-811-15/c
; Sequence 15, Application US/10361811
; Publication No. US20030206918A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C8
; CURRENT APPLICATION NUMBER: US/10/361,811
; CURRENT FILING DATE: 2003-02-05
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 333
; OTHER INFORMATION: n = A,T,C or G
US-10-361-811-15

Query Match      100.0%; Score 21; DB 13; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGTCTGGTC 21
   |||||
Db 145 ATTGCTGAGACCGTCTGGTC 125

RESULT 9
US-10-212-677-15/c
; Sequence 15, Application US/10212677
; Publication No. US20030129192A1
; GENERAL INFORMATION:
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212,677
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 333
; OTHER INFORMATION: n = A,T,C or G
US-10-212-677-15

Query Match      100.0%; Score 21; DB 16; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.58;
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGTCTGGTC 21
|||||
Db 145 ATTGCTGAGACCGTCTGGTC 125

RESULT 10

US-09-918-995-32172/c
; Sequence 32172, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32172
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(461)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-32172

Query Match 100.0%; Score 21; DB 11; Length 461;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGTCTGGTC 21
|||||
Db 196 ATTGCTGAGACCGTCTGGTC 176

RESULT 11

US-09-918-995-2524/c
; Sequence 2524, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2524
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(462)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-2524

Query Match 100.0%; Score 21; DB 11; Length 462;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGTCTGGTC 21
|||||
Db 181 ATTGCTGAGACCGTCTGGTC 161

RESULT 12

US-09-918-995-32177/c
; Sequence 32177, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32177
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(465)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-32177

Query Match 100.0%; Score 21; DB 11; Length 465;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGTCTGGTC 21
|||||
Db 188 ATTGCTGAGACCGTCTGGTC 168

RESULT 13

US-09-918-995-31156/c
; Sequence 31156, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31156
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(492)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-31156

Query Match 100.0%; Score 21; DB 11; Length 492;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGTCTGGTC 21
|||||
Db 174 ATTGCTGAGACCGTCTGGTC 154

RESULT 14

US-09-833-381-910/c
; Sequence 910, Application US/09833381

; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 910
; LENGTH: 532
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(532)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-910

Query Match 100.0%; Score 21; DB 10; Length 532;
Best Local Similarity 100.0%; Pred. No. 0.58; 0; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATTCTCTGAGACCGCTGTGGTC 21
|||||
Db 159 ATTCTCTGAGACCGCTGTGGTC 139

RESULT 15

US-09-918-995-31688/C
; Sequence 31688, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31688
; LENGTH: 539
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(539)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-31688

Query Match 100.0%; Score 21; DB 11; Length 539;
Best Local Similarity 100.0%; Pred. No. 0.58; 0; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATTCTCTGAGACCGCTGTGGTC 21
|||||
Db 207 ATTCTCTGAGACCGCTGTGGTC 187

Search completed: January 21, 2004, 15:35:43
Job time : 224 secs

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GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 10:07:51 ; Search time 799.5 Seconds
(without alignments)
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US-09-913-325-12

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Perfect score: 21
Sequence: 1 gctggcgagtggtgggggct 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

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6: gb_pat.*

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12: gb_sy.*

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14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rtd.*

36: em_htg_vrt.*

37: em_htg_mam.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	21	100.0	975	6	AX014321	Sequence
C 2	21	100.0	1416	6	AX014321	Sequence
C 3	21	100.0	1416	9	AR270755	Sequence
C 4	21	100.0	1416	9	M74816	Human sulfa
C 5	21	100.0	1512	6	AX302541	Sequence
C 6	21	100.0	1512	9	AX302541	Sequence
C 7	21	100.0	1512	9	AX302541	Sequence
C 8	21	100.0	1512	9	AX302541	Sequence
C 9	21	100.0	1512	9	AX302541	Sequence
C 10	21	100.0	1512	9	AX302541	Sequence
C 11	21	100.0	1512	9	AX302541	Sequence
C 12	21	100.0	1512	9	AX302541	Sequence
C 13	21	100.0	1512	9	AX302541	Sequence
C 14	21	100.0	1512	9	AX302541	Sequence
C 15	21	100.0	1512	9	AX302541	Sequence
C 16	21	100.0	1512	9	AX302541	Sequence
C 17	21	100.0	1512	9	AX302541	Sequence
C 18	21	100.0	1512	9	AX302541	Sequence
C 19	21	100.0	1512	9	AX302541	Sequence
C 20	21	100.0	1512	9	AX302541	Sequence
C 21	18.4	87.6	57722	2	HSCB33810	Sequence
C 22	18.4	87.6	57722	2	HSCB33810	Sequence
C 23	18.4	87.6	57722	2	HSCB33810	Sequence
C 24	18.4	87.6	57722	2	HSCB33810	Sequence
C 25	17.8	84.8	147895	9	AC079171	Sequence
C 26	17.8	84.8	147895	9	AC079171	Sequence
C 27	17.8	84.8	147895	9	AC079171	Sequence
C 28	17.8	84.8	147895	9	AC079171	Sequence
C 29	17.8	84.8	147895	9	AC079171	Sequence
C 30	17.8	84.8	147895	9	AC079171	Sequence
C 31	17.8	84.8	147895	9	AC079171	Sequence
C 32	17.8	84.8	147895	9	AC079171	Sequence
C 33	17.8	84.8	147895	9	AC079171	Sequence
C 34	17.8	84.8	147895	9	AC079171	Sequence
C 35	17.8	84.8	147895	9	AC079171	Sequence
C 36	17.8	84.8	147895	9	AC079171	Sequence
C 37	17.8	84.8	147895	9	AC079171	Sequence
C 38	17.8	84.8	147895	9	AC079171	Sequence
C 39	17.8	84.8	147895	9	AC079171	Sequence
C 40	17.4	82.9	3545	6	AX505167	Sequence
C 41	17.4	82.9	3545	6	AX505167	Sequence
C 42	17.4	82.9	3545	6	AX505167	Sequence
C 43	17.4	82.9	3545	6	AX505167	Sequence
C 44	17.4	82.9	3545	6	AX505167	Sequence
C 45	17.4	82.9	3545	6	AX505167	Sequence

ALIGNMENTS

RESULT 1	AX014321/c	AX014321	975 bp	DNA	linear	PAT 07-SEP-2000
LOCUS	Sequence 29 from Patent WO954353.					
DEFINITION	Sequence 29 from Patent WO954353.					
ACCESSION	AX014321					
VERSION	AX014321.1	GI:10040675				
KEYWORDS	Homo sapiens (human)					
SOURCE	Homo sapiens					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.					
TITLE	Schmitt, A., Specht, T., Dahl, E., Hinzmann, B., Rosenthal, A. and					
	Pilarsky, C.					
	Human nucleic acid sequences of normal uterus tissue					

Pred. No. is the number of results predicted by chance to have a

JOURNAL Patent: WO 9954353-A 29 28-OCT-1999;
SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN
(DE); PILARSKY CHRISTIAN (DE)

FEATURES
source
1. .975
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 221 a 320 c 248 g 186 t

ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 975;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCGGAGTTGGGGCCT 21
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Db 903 GCTGGCGGAGTTGGGGCCT 883
|||||

RESULT 2
AR270755/c
LOCUS 1416 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 1318 from patent US 6500938.
ACCESSION AR270755
VERSION AR270755.1 GI:29701989
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1416)
AUTHORS Au-Young, J. and Seilhamer, J.J.
TITLE Composition for the detection of signaling pathway gene expression
JOURNAL Patent: US 6500938-A 1318 31-DEC-2002;
FEATURES
source
1. .1416
/organism="unknown"

BASE COUNT 344 a 440 c 365 g 267 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 46;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCGGAGTTGGGGCCT 21
|||||

Db 1309 GCTGGCGGAGTTGGGGCCT 1289
|||||

RESULT 3
HUMSGLY/c
LOCUS 1416 bp mRNA linear PRI 09-JAN-1995
DEFINITION Human sulfated glycoprotein-2 mRNA, 3' end.
ACCESSION M74816
VERSION M74816.1 GI:338056
KEYWORDS secreted protein; sulfated glycoprotein-2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Danik, M., Chabot, J.-G., Mercier, C., Benabid, A.L., Chauvin, C.,
Quirion, R. and Suh, M.
TITLE Human gliomas and epileptic foci express high levels of a mRNA
related to rat testicular sulfated glycoprotein 2, a purported
marker of cell death
Proc. Natl. Acad. Sci. U.S.A. 88 (19), 8577-8581 (1991)
JOURNAL 92020896
MEDLINE 1924317
PUBMED
COMMENT Original source text: Homo sapiens male 63 yr. old adult brain
tumor cDNA to mRNA.
FEATURES
Location/Qualifiers

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1. .1416
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/map="8"
/sex="male"
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/tissue_type="brain tumor"
/dev_stage="63 yr. old adult"

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1. .1416
/gene="CLI"

CDS
c1. .1172
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/protein_id="AAA60321.1"
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TMMALWBECKPCLKQTCMKFYARVCVSGSLVGRQLEEFNQSPFFYFMNGDRIDSL
LENDROQTHMLDVMDHFGRASSIIDLEFQDRFFFTREPQDTHYLPFSLPHRRPHFF
PKSRIVRSILMPFSPYEPLNFHAMFQPFLEMIHEAQAMDIFHSFAFQHPHTEFIREG
DDRTVCEIRHNSCTCLMKQCDKCRILSVDCSTNNPSOAKLRREDESLQVAERS
LFEKYNELLSYQWKMLNTSLLEOLNEQFNVRSLANTQGEDOYVLEVTVAHS
DSDVSGVTEVVVKLFDSDPITVTTFVPSVRKPKPMETVAEKALQETAKKHEE"

BASE COUNT 344 a 440 c 365 g 267 t

ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 1416;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCGGAGTTGGGGCCT 21
|||||

Db 1309 GCTGGCGGAGTTGGGGCCT 1289
|||||

RESULT 4
AX302541/c
LOCUS 1512 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 59 from Patent WO0175177.
ACCESSION AX302541
VERSION AX302541.1 GI:17383080
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Morin, P.J., Sherman-Baust, C.A., Pizer, E.S. and Hough, C.D.
TITLE Tumor markers in ovarian cancer
JOURNAL Patent: WO 0175177-A 59 11-OCT-2001;
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)

FEATURES
source
1. .1512
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 378 a 461 c 387 g 286 t

ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 1512;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCGGAGTTGGGGCCT 21
|||||

Db 1405 GCTGGCGGAGTTGGGGCCT 1385
|||||

RESULT 5
HUMAPOJ/c
LOCUS 1512 bp mRNA linear PRI 31-OCT-1994

```

DEFINITION Human apolipoprotein J mRNA, complete cds.
ACCESSION J02908
VERSION J02908.1 GI:1178854
KEYWORDS apolipoprotein J; high density lipoprotein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1512)
AUTHORS de Silva,H.V., Harmony,J.A., Stuart,W.D., Gil,C.M. and Robbins,J.
TITLE Apolipoprotein J: structure and tissue distribution
JOURNAL Biochemistry 29 (22), 5380-5389 (1990)
MEDLINE 90344779
PUBMED 1974459
COMMENT Original source text: Human fetal liver, cDNA to mRNA, clone
lambda[1-3].
Draft entry and computer-readable sequence for [1] kindly submitted
by J.Robbins, 21-MAR-1990.
FEATURES
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     /map="Unassigned"
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     /gene="APOJ"
     /product="apolipoprotein J mRNA"
     18..1268
     /gene="APOJ"
     /note="apolipoprotein J precursor"
     /codon_start=1
     /protein_id="AAA51765.1"
     /db_xref="GI:178855"
     /db_xref="GDB:13053"
     /translation="MSNGSKYVKNKEIQNAVGVKQIKTLIEKTEERKTLNLEEA
KKKEDALNETRESTKIKELPGVNCETMALWECKPCIKQTKWKFVYVRCGSGL
VGRQLEELNGSSPYFWNGDRIDSLLENDQQOQMLDVQDHFSSASSIDSLFQD
RFTPEQQTTHYLFSPDHPHPFPFKSLVSLSPSPSPSPSPSPSPSPSPSPSPSPSP
HEAQQADHIFSPAFQHPPTFEFIREGDDRTVCRHINSTGICRKKQCDKCREIL
SVDCSTNPFSQAKLRLEDSQVAERLTRKYNELLSQWMLNTSLLEQLNEQFN
WYSRLANLTQGEDQYLVRLVTVVASHTSDSVPSTGVTVVVKLFDSDPITVTPVEVSR
KNPKFMTVAEKALQYRKKHREE"
mat_peptide
18..599
/gene="APOJ"
/product="apolipoprotein J alpha-subunit"
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/gene="APOJ"
/product="apolipoprotein J beta-subunit"
BASE COUNT 378 a 461 c 367 g 286 t
ORIGIN
Query Match 100.0%; Score 21; DB 9; Length 1512;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCTGGCGGAGTTGGGGGCT 21
Db 1405 GCTGGCGGAGTTGGGGGCT 1385
RESULT 6
AK093399/c
LOCUS AK093399 1546 bp mRNA linear PRI 15-JUL-2002
DEFINITION Homo sapiens cDNA FLJ36080 fis, clone TEST12019872, highly similar
to CLUSTERIN PRECURSOR.
ACCESSION AK093399
VERSION AK093399.1 GI:21752259
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1546)
AUTHORS Isogai,T. and Yamamoto,J.
TITLE Direct Submission
JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomeshri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1423 GCTGGCGGAGTTGGGGGCT 1403
RESULT 7
AK093399/c
LOCUS AK093399 1648 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 3 from patent US 6383808.
ACCESSION AK093399
VERSION AK093399.1 GI:21509928
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1648)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 3 07-MAY-2002;
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Best Local Similarity 100.0%; Pred. No. 45;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCTGGCGGAGTTGGGGGCT 21
Db 1541 GCTGGCGGAGTTGGGGGCT 1521

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RESULT 8
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LOCUS HUMTRPM2A 1648 bp mRNA linear PRI 23-AUG-1996
DEFINITION Human TRPM-2 mRNA, complete cds.
ACCESSION M64722
VERSION M64722.1 GI:3339972
KEYWORDS TRPM-2 protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
1 (sites)
Wong, P., Pineault, J., Lakins, J., Taillefer, D., Leger, J., Wang, C.
and Tenniswood, M.
Genomic organization and expression of the rat TRPM-2 (clusterin)
gene, a gene implicated in apoptosis
J. Biol. Chem. 268 (7), 5021-5031 (1993)
93186813
7680346
2 (bases 1 to 1648)
Wong, P., Taillefer, D., Lakins, J., Pineault, J., Chader, G. and
Tenniswood, M.
Molecular characterization of human TRPM-2/clusterin, a gene
associated with sperm maturation, apoptosis and neurodegeneration
Eur. J. Biochem. 221 (3), 917-925 (1994)
94237156
8181474
PUBMED
COMMENT Original source text: Human cDNA to mRNA.
FEATURES
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FFPKSRIVSLMFPSPYEPFLNFHAMQPELEHQAQQAMDIFHSFAFQHPPTFFIR
EGDDRTVCREIRHNSGTCLRMKQDCKREILSDVCSNTNPSQAKLRRELDLSQVA
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BASE COUNT 408 a 488 c 440 g 312 t
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Best Local Similarity 100.0%; Pred. No. 45;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTGGCGGAGTGGGGGCT 21
Db 1541 GCTGGCGGAGTGGGGGCT 1521
RESULT 9
BC019588/c
LOCUS BC019588 1658 bp mRNA linear PRI 17-APR-2003
DEFINITION Homo sapiens clusterin (complement lysis inhibitor, SP-40,40,
sulfated glycoprotein 2, testosterone-repressed prostate message 2,
apolipoprotein J), mRNA (cDNA clone MGC:24903 IMAGE:4915444),
complete cds.
ACCESSION BC019588
VERSION BC019588.1 GI:18043614

KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1658)
STRAUSBERG, R.L., Feingold, E.A., Grouse, L.H., Derge, J.M., Schuler, G.D.,
Klauser, R.D., Collins, F.S., Wagner, L., Shenman, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M.E., Brownstein, M.J., Udén, T.B., Toshyuki, S.,
Schecter, T.E., Brownstein, M.J., Udén, T.B., Toshyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shavchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Snailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 1658)
STRAUSBERG, R.
Direct Submission
Submitted (19-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Lounseged, H.,
Kowis, C.R., Sheed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 29 Row: m Column: 21
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4502904.
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EGDDRTVCREIRHNSTGCLRMKQDCKREILSVDCSTNNPSQAKLRRELDLSQVA
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BASE COUNT 423 a 486 c 439 g 310 t
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Query Match 100.0%; Score 21; DB 9; Length 1658;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCGGAGTTGGGGCCCT 21
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Db 1535 GCTGGCGGAGTTGGGGCCCT 1515

RESULT 10
HSCSP40/c
LOCUS HSCSP40 1676 bp mRNA linear PRI 22-MAR-1995
DEFINITION Human SP-40,40 mRNA for complement-associated protein SP-40,40
alpha-1 and beta-1 chain.
ACCESSION X14723
VERSION X14723.1 GI:30250
KEYWORDS complement-associated protein; serum protein; SP-40,40 gene.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1676)
AUTHORS Kirschbaum, L., Sharpe, J.A., Murphy, B., d'Apice, A.J., Classon, B.,
Hudson, P. and Walker, I.D.
TITLE Molecular cloning and characterization of the novel, human
complement-associated protein, SP-40,40: a link between the
complement and reproductive systems
JOURNAL EMBO J. 8 (3), 711-718 (1989)
MEDLINE 89251601
FURNED 2721499
REFERENCE 2 (bases 1 to 1676)
AUTHORS Kirschbaum, L.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1989) Kirschbaum L., The University of Melbourne,
The Preclinical Centre, School of Veterinary Science, Parkville
Victoria 3052, Australia
COMMENT The sequence overlaps with that reported by Murphy et. al. in J.
Clin. Invest. 81:1858-1864(1988).
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message 2, apolipoprotein J)"
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BASE COUNT 423 a 486 c 439 g 310 t
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Best Local Similarity 100.0%; Pred. No. 45;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCGGAGTTGGGGCCCT 21
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Db 1535 GCTGGCGGAGTTGGGGCCCT 1515

RESULT 11
LOCUS AX202086 1678 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 16 from Patent WO0153531.
ACCESSION AX202086
VERSION AX202086.1 GI:15391872
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Phippard, D., Vasanthakumari, G., Dotson, S. and Ma, X.J.
TITLE Osteoarthritis tissue derived nucleic acids, polypeptides, vectors,
and cells
JOURNAL Patent: WO 0153531-A 16 26-JUL-2001;
Pharmacia Corporation (US)
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Best Local Similarity 100.0%; Pred. No. 45;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCGGAGTTGGGGCCCT 21
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Db 1558 GCTGGCGGAGTTGGGGCCCT 1538

RESULT 12
LOCUS BC010514 1684 bp mRNA linear PRI 17-APR-2003
DEFINITION Homo sapiens clusterin (complement lysis inhibitor, SP-40,40,
sulfated glycoprotein 2, testosterone-repressed prostate message 2,
apolipoprotein J), mRNA (cDNA clone MGC:18080 IMAGE:4150452),
complete cds.
ACCESSION BC010514
VERSION BC010514.1 GI:14714740
KEYWORDS MGC.
SOURCE Homo sapiens (human)

```

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1684)
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, S., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.E., Bonaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
 Carninci, P., Prange, C., Raja, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, R.D., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
 Villalón, D.K., Muzny, D.N., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalitus, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 2388257
 12477932
 2 (bases 1 to 1684)
 Strausberg, R.
 Direct Submission
 Submitted (10-JUL-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabs-x@mail.nih.gov
 Tissue Procurement: David N. Louis, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louis, H.,
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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 SLENDROTHMLDVMQHFSSASSIDELFQDRFFTRFQDTHIFFSLPHKRPFR
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 Query Match 100.0%; Score 21; DB 9; Length 1684;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTGGCGGAGTTGGGGCCT 21
 Db 1555 GCTGGCGGAGTTGGGGCCT 1535
 RESULT 13
 AX330207/c
 LOCUS AX330207 3196 bp DNA linear PAT 09-JAN-2002
 DEFINITION Sequence 716 from Patent WO0194629.
 ACCESSION AX330207
 VERSION AX330207.1 GI:18103185
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
 Horrigan, S., Soppet, D.R. and Weaver, Z.
 Cancer gene determination and therapeutic screening using signature
 gene sets
 JOURNAL Patens: WO 0194629-A 716 13-DEC-2001;
 Avalon Pharmaceuticals (US)
 FEATURES
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 QY 1 GCTGGCGGAGTTGGGGCCT 21
 Db 2891 GCTGGCGGAGTTGGGGCCT 2871
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 AX337122/c
 LOCUS AX337122 3196 bp DNA linear PAT 09-JAN-2002
 DEFINITION Sequence 7631 from Patent WO0194629.
 ACCESSION AX337122
 VERSION AX337122.1 GI:18127841
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
 Horrigan, S., Soppet, D.R. and Weaver, Z.
 Cancer gene determination and therapeutic screening using signature

EGDDRTVCREIRHSTGCLRMKODCKREILSVDCSTNNPSQAKRLRELDSELSQVA
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 42;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTGGCGGAGTTGGGGCCT 21
DB 2891 GCTGGCGGAGTTGGGGCCT 2871
Search completed: January 21, 2004, 12:11:48
Job time : 805 secs

gene sets
Patent: WO 0194629-A 7631 13-DEC-2001;
Avalon Pharmaceuticals (US)
Location/Qualifiers
1..3196
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 833 a 762 c 789 g 812 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 42;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTGGCGGAGTTGGGGCCT 21
DB 2891 GCTGGCGGAGTTGGGGCCT 2871
RESULT 15
HUMTRPM2A4/c
LOCUS Human TRPM-2 protein gene, exons 7,8,9 and complete cds.
DEFINITION
ACCESSION M63379.1 GI:292841
VERSION TRPM-2 protein.
KEYWORDS 4 of 4
SEGMENT
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (sites)
Wong, P., Pineault, J., Lakins, J., Taillefer, D., Leger, J., Wang, C.
and Tenniswood, M.
Genomic organization and expression of the rat TRPM-2 (clusterin)
gene, a gene implicated in apoptosis
J. Biol. Chem. 268 (7), 5021-5031 (1993)
93186813
7680346
2 (bases 1 to 3196)
Wong, P., Taillefer, D., Lakins, J., Pineault, J., Chader, G. and
Tenniswood, M.
Molecular characterization of human TRPM-2/clusterin, a gene
associated with sperm maturation, apoptosis and neurodegeneration
Eur. J. Biochem. 221 (3), 917-925 (1994)
94237156
8181474
COMMENT
Original
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1..3196
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/mol_type="genomic DNA"
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1..3166)
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M63376.1:7021..7169,M63377.1:155..325,M63378.1:308..719,
M63378.1:1247..1351,995..1224,2362..2537,2745..2998)
/gene="TRPM-2"
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M63377.1:155..325,M63378.1:308..719,M63378.1:1247..1351,
995..1224,2362..2537,2745..2754)
/gene="TRPM-2"
/codon_start=1
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NETWALWESCKLQTCWKVYVRCVSGSLVGRQLEEFNQSSPFYFMNGGRID
SLLENDROQTHLDVMDQHSRASSIIDLFDQRPFTREPDYHYLPSPFLRRPHF
FFPKSRIVSLMFFSPYELNFMFQPLEMHEAQQAQMDIHFPSPAPCHPPTFRIF

FEATURES
source
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CDS

FEATURES
source
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CDS

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 10:04:17 ; Search time 148 Seconds
(without alignments)
383.028 Million cell updates/sec

Title: US-09-913-325-12
Perfect score: 21
Sequence: 1 gctggcgagtggtggggcct 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues
Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
- 25: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	AAA94234	Human testosterone
2	21	100.0	975	AAZ4353	Human normal uteru
3	21	100.0	1416	ACA56720	Human signalling p
4	21	100.0	1512	ASA83111	Apolipoprotein J o
5	21	100.0	1648	AEN98656	Human clusterin ge
6	21	100.0	1678	AAH23086	Osteoarthritis tis
7	21	100.0	2876	AAAC90467	Human uncoupling p
8	21	100.0	3196	ABL62379	Colon adenocarcino

C 9	21	100.0	3196	24	ABL62994	Prostate cancer re
C 10	21	100.0	8133	24	ABN99663	Human clusterin ge
C 11	17.8	84.8	250	24	ABL80072	Human ovarian can
C 12	17.4	82.9	3845	24	ABQ94233	FL011 gene express
C 13	17.4	82.9	3732	24	ABQ94271	Fungal gene expres
C 14	16.8	80.0	2137	25	ABZ57220	Human zinc finger
C 15	16.8	80.0	2535	24	AAH25134	Nucleotide sequenc
C 16	16.8	80.0	2535	24	ABX15715	Human 21612 alcoho
C 17	16.8	80.0	2962	20	AAK28161	Rat Acid sensitive
C 18	16.8	80.0	3562	19	AAV60839	Rat acid sensing i
C 19	16.8	80.0	3562	21	AAZ61197	CDNA encoding a ra
C 20	16.8	80.0	3647	19	AAV60842	Rat acid sensing i
C 21	16.8	80.0	3647	21	AAZ61200	CDNA encoding a ra
C 22	16.8	80.0	4121	21	AACT5317	Human ORFX ORF872
C 23	16.8	80.0	4196	25	ABX71009	Novel human cDNA s
C 24	16.8	80.0	4342	25	ABX08824	Angiogenesis-assoc
C 25	16.8	80.0	4344	25	AAZ53171	Human kinases and
C 26	16.8	80.0	14854	22	AAZ28620	Genomic sequence #
C 27	16.8	80.0	349980	24	ABQ81849	Biifidobacterium lo
C 28	16.4	78.1	50	15	AAQ69840	Simian virus 40 T/
C 29	16.4	78.1	50	18	AAAT64302	SV40 T/t late (sta
C 30	16.4	78.1	50	20	ABX17590	Test sequence from
C 31	16.4	78.1	50	24	ABK83081	DNA binding molecu
C 32	16.4	78.1	58	20	AAV64746	HIV anti-viral oli
C 33	16.4	78.1	68	22	AAH24758	Nucleotide sequenc
C 34	16.4	78.1	144	25	ABZ79849	Simian virus 40 ea
C 35	16.4	78.1	185	10	AAAN0660	Sequence of SV40 e
C 36	16.4	78.1	204	21	AAAI2021	Murine lactate deh
C 37	16.4	78.1	223	21	AAAI2017	Human enolase A pr
C 38	16.4	78.1	226	24	ABU53832	SV40 promoter. Rh
C 39	16.4	78.1	226	24	ABU53845	SV40 promoter sequ
C 40	16.4	78.1	231	21	AACT73859	Murine PGK HRE der
C 41	16.4	78.1	237	21	AAAI2001	Promoter OBHrel us
C 42	16.4	78.1	242	20	AAZ07789	Murine PGK HRE der
C 43	16.4	78.1	242	21	AAAI2016	Murine PGK fragmen
C 44	16.4	78.1	243	20	AAZ11397	Murine PGK HRE der
C 45	16.4	78.1	243	21	AAAI1995	

ALIGNMENTS

RESULT 1

- AAA94234
- ID AAA94234 standard; DNA; 21 BP.
- XX AAA94234;
- AC AAA94234;
- XX AAA94234;
- DT 12-JAN-2001 (first entry)
- XX Human testosterone-repressed prostate message-2 antisense oligo #10.
- DE Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;
- XX Human; testosterone-repressed prostate message-2; SGP-2; cancer; antisense oligonucleotide; ss.
- KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.
- XX Homo sapiens.
- OS Homo sapiens.
- XX WO200049937-A2.
- EN WO200049937-A2.
- XX 31-AUG-2000.
- XX 25-FEB-2000; 2000WO-US04875.
- XX 26-FEB-1999; 99US-0121726.
- XX (UYBR-) UNIV BRITISH COLUMBIA.
- PA Gleave M, Rennie FS, Miyake H, Nelson C;
- XX WPI; 2000-533132/48.
- XX Treating prostatic tumors and renal cancers by antisense inhibition of
- PT the testosterone-repressed prostate messenger-2 gene -

XX PS Example 5; Page 38; 38pp; English.

XX CC The present sequence is an antisense oligonucleotide directed at the
XX CC human testosterone-repressed prostate message-2 (TRPM-2, also known as
XX CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to
XX CC promote the regression of tumors, and oligonucleotides directed
XX CC at human TRPM-2 can be used in the treatment of tumour cells expressing
XX CC the TRPM-2 gene. These include prostate cancer, renal cell cancer and
XX CC some breast cancer cells. In addition to this, they also increase the
XX CC chemosensitivity of the cells, meaning that conventional chemotherapy is
XX CC more effective.

XX SQ Sequence 21 BP; 1 A; 4 C; 12 G; 4 T; 0 other;

Query Match 100.0%; Score 21; DB 21; Length 21;
Best Local Similarity 100.0%; Pred. NO. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q/ 1 GCTGGCGGAGTTGGGGCCT 21

Db 1 GCTGGCGGAGTTGGGGCCT 21

RESULT 2

AAZ41353/c

ID AAZ41353 standard; cDNA; 975 BP.

XX AC AAZ41353;

XX DT 19-JAN-2000 (first entry)

XX DE Human normal uterus tissue derived cDNA 29.

XX KW Human; uterus; cancer; treatment; anticancer; cytostatic; gene therapy;
XX KW EST; expressed sequence tag; ss.

XX OS Homo sapiens.

XX FN DEL9817946-A1.

XX PD 21-OCT-1999.

XX PF 17-APR-1998; 98DE-1017946.

XX PR 17-APR-1998; 98DE-1017946.

XX PA (META-) METAGEN GES GENOMFORSCHUNG MBH.

XX PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;

XX WPI; 1999-591956/51.

XX CC New nucleic acid sequences expressed in normal uterine tissues, and
XX CC derived polypeptides, for treatment of uterine cancer and
XX CC identification of therapeutic agents -

XX PS Claim 3; Page 95; 154pp; German.

XX CC This invention describes novel cDNA sequences (A) highly expressed in
XX CC normal uterine tissue which can have anticancer and cytostatic activity
XX CC and can be used for gene therapy. (A) are used (i) for recombinant
XX CC expression of polypeptides (B) and (ii) to isolate complete genes.
XX CC (B) are used (i) to identify agents suitable for treatment of uterine
XX CC cancer; (ii) directly for treating this form of cancer (including
XX CC expression from gene therapy vectors) and (iii) for generation of
XX CC specific antibodies. (A) are identified by assembling ESTs (expressed
XX CC sequence tags) from a particular tissue type before comparison of the
XX CC expression patterns. This allows a significantly longer fragment of the
XX CC gene to be revealed, so should reduce the number of failures associated
XX CC with the fact that ESTs from different libraries may represent
XX CC different parts of the same unknown gene, distorting the estimated
XX CC frequency of occurrence in a particular tissue. AAZ41325-241385

CC represent the human uterine tissue derived cDNA fragments of the
CC invention which encode the protein fragments represented in
CC CC AAY59838-Y59892.

XX SQ Sequence 975 BP; 221 A; 320 C; 248 G; 186 T; 0 other;

Query Match 100.0%; Score 21; DB 20; Length 975;
Best Local Similarity 100.0%; Pred. NO. 13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q/ 1 GCTGGCGGAGTTGGGGCCT 21

Db 903 GCTGGCGGAGTTGGGGCCT 883

RESULT 3

ACA56720/c

ID ACA56720 standard; cDNA; 1416 BP.

XX AC ACA56720;

XX DT 06-JUN-2003 (first entry)

XX DE Human signalling pathway polynucleotide probe SEQ ID NO 1318.

XX KW Human; probe; ss; array element; Parkinson's disease;

XX KW signalling pathway population; cancer; adenocarcinoma; leukaemia;

XX KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.

XX OS Homo sapiens.

XX PN US6500938-B1.

XX PD 31-DEC-2002.

XX PF 30-JAN-1998; 98US-0016434.

XX PR 30-JAN-1998; 98US-0016434.

XX PA (INCY-) INCYTE GENOMICS INC.

XX PI Au-Young J, Seilhamer JJ;

XX WPI; 2003-352189/33.

XX CC Combination of polynucleotide probes, useful as array elements in a
XX CC microarray for monitoring the expression of a number of target
XX CC polynucleotides -

XX PS Claim 1; SEQ ID NO 1318; 65pp; English.

XX CC The invention relates to a combination which, comprises a number of
XX CC polynucleotide probes comprising a sequence selected from one of the 1490
XX CC sequences mentioned in the specification. The combination is useful as an
XX CC array element in a microarray for monitoring the expression of a number
XX CC of target polynucleotides. The microarray is particularly useful in the
XX CC diagnosis and treatment of cancer and immunopathology and neuropathology.
XX CC The microarray is useful in diagnostics and treatment regimens, drug
XX CC discovery and pharmacogenomics. The microarray is also useful for
XX CC profiling the effects of currently available therapeutic drugs. The
XX CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
XX CC and genomic fragments and in research and diagnostic applications. The
XX CC array can detect changes in expression in a large number of genes coding
XX CC for different signaling pathway populations which can be used to diagnose
XX CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
XX CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
XX CC and Parkinson's disease. The present sequence represents a polynucleotide
XX CC probe of the invention.
XX CC Note: the sequence data for this patent did not form part of the printed
XX CC specification but was obtained in electronic format directly from USPTO
XX CC at seqdata.uspto.gov/sequence.html?DocID=96500938B1.

CC tumour. The ovarian tumour marker genes of the invention were identified
CC using SAGE (serial analysis of gene expression) and were found to be
CC overexpressed in a broad variety of ovarian epithelial tumour cells
CC relative to normal ovarian epithelial cells. The marker genes are
CC implicated in immune response pathways, in the regulation of cell
CC proliferation and in protein folding, and many of these are membrane-
CC localised or secreted. In addition to their use as diagnostic and
CC prognostic markers, the ovarian tumour marker genes or their encoded
CC proteins may be used as therapeutic targets for the treatment and
CC prevention of ovarian cancer. Sequences ABA83081-ABA83122, ABA83180,
CC ABA83182 and ABA83184 represent the ovarian tumour marker genes of
CC the invention.

XX SQ Sequence 1512 BP; 378 A; 461 C; 387 G; 286 T; 0 other;

Query Match 100.0%; Score 21; DB 22; Length 1512;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCGGAGTTGGGGCCT 21
|||||

Db 1405 GCTGGCGGAGTTGGGGCCT 1385
|||||

RESULT 5
ABN99656/c
ID AEN99656 standard; DNA: 1648 BP.
XX AC AEN99656;
XX DT 16-AUG-2002 (first entry)
XX DE Human clusterin gene sequence 1.
XX KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
XX KW hypercholesterolaemia; cardiovascular disorder; ds;
XX KW hyperproliferative disorder; hyperlipidemic disorder.
XX OS Homo sapiens.
XX PN WO200222635-A1.
XX PD 21-MAR-2002.
XX PF 10-SEP-2001; 2001WO-US28235.
XX PR 11-SEP-2000; 2000US-0659791.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM;
XX DR WPI; 2002-404805/43.
XX DR P-PSDB; AAO15039.
XX PT Novel antisense compound targeted to nucleic acid molecule encoding
XX clusterin, useful for treating animal having disease associated with
XX clusterin such as hyperlipidemic disorder, cardiovascular disorder -
XX Example 13; Page 89-92; 125pp; English.
XX CC The invention comprises antisense oligonucleotides that are capable of
XX inhibiting expression of the human clusterin gene. The antisense
XX oligonucleotides of the invention are useful for inhibiting the
XX expression of clusterin in cells. The antisense oligonucleotides are also
XX useful for treating an animal with a disease or condition associated with
XX clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
XX hyperproliferative disorders; and hyperlipidemic disorders). The present
XX DNA sequence represents a human clusterin gene sequence.
XX SQ Sequence 1648 BP; 408 A; 488 C; 440 G; 312 T; 0 other;

Query Match 100.0%; Score 21; DB 24; Length 1648;

XX SQ Sequence 1416 BP; 344 A; 440 C; 365 G; 267 T; 0 other;

Query Match 100.0%; Score 21; DB 25; Length 1416;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCGGAGTTGGGGCCT 21
|||||

Db 1309 GCTGGCGGAGTTGGGGCCT 1289
|||||

RESULT 4
ABA83111/c
ID ABA83111 standard; DNA: 1512 BP.
XX AC ABA83111;
XX DT 08-FEB-2002 (first entry)
XX DE Apolipoprotein J ovarian tumour marker gene, SEQ ID NO:59.
XX KW Ovarian tumour marker gene; human; overexpression; upregulation;
XX KW epithelial tumour; cancer; diagnosis; prognosis; disease monitoring;
XX KW identification; serous cystadenoma; borderline serous tumour;
XX KW serous cystadenocarcinoma; mucinous cystadenocarcinoma;
XX KW mucinous cystadenoma; borderline mucinous tumour; endometrioid carcinoma;
XX KW undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma;
XX KW adenofibroma; Brenner tumour; serial analysis of gene expression; SAGE;
XX KW immune response pathway; cell proliferation regulation; protein folding;
XX KW membrane localised; secreted; therapeutic target; cytostatic;
XX KW gene therapy; vaccine; ds.
XX OS Homo sapiens.
XX PN WO200175177-A2.
XX PD 11-OCT-2001.
XX PF 03-APR-2001; 2001WO-US10947.
XX PR 03-APR-2000; 2000US-194336P.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Morin PJ, Sherman-Baust CA, Pizer ES, Hough CD;
XX DR WPI; 2001-626450/72.
XX DR P-PSDB; ABB50285.
XX PT Detecting and identifying ovarian tumor, identifying increased risk for
XX developing ovarian cancer, and determining effectiveness of ovarian
XX cancer treatment, by measuring expression level of ovarian tumor marker
XX gene -
XX Claim 23; Page 103; 140pp; English.
XX CC The invention relates to methods for diagnosing and prognosing ovarian
XX tumours in an individual via the detection and measurement of the
XX expression of ovarian tumour marker genes (ABA83081-ABA83122, ABA83180,
XX ABA83182 and ABA83184) or segments thereof (ABA83123-ABA83169, ABA83179,
XX ABA83181 and ABA83183). The methods of the invention are useful for
XX detecting an ovarian tumour in a patient, for identifying an individual
XX at increased risk for developing ovarian cancer, in prognostic tests for
XX assessing the relative severity of ovarian cancer, in tests for
XX monitoring a patient in remission from ovarian cancer and in tests for
XX monitoring disease status in a patient being treated for ovarian cancer.
XX The methods can additionally be used to identify a particular tumour as
XX being an ovarian tumour (i.e., an epithelial ovarian tumour selected from
XX serous cystadenoma, borderline serous tumour, serous cystadenocarcinoma,
XX mucinous cystadenoma, endometrioid carcinoma, undifferentiated carcinoma,
XX clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner.

XX	12-MAR-2001	(first entry)	
DT	Human uncoupling protein cDNA #16.		
XX			
DE	Human uncoupling protein; immunosuppressive; antiarthritic;		
XX	antirheumatic; antiproliferative; cardiac; vasotropic;		
DE	cerboprotective; neuroprotective; antibacterial; ophthalmological;		
KW	gastrointestinal; nephrotropic; gynaecological; vulnary; thrombolytic;		
KW	gene therapy; cancer; wound; infectious disease; thrombosis; arthritis;		
KW	infertility; ss.		
XX			
OS	Homo sapiens.		
XX			
WO	WO200061614-A2.		
XX			
PD	19-OCT-2000.		
XX			
PF	06-APR-2000; 2000WO-US09534.		
XX			
PR	09-APR-1999; 99US-0128701.		
XX			
PR	08-JUL-1999; 99US-0142821.		
XX			
PR	18-AUG-1999; 99US-0149448.		
XX			
PR	12-NOV-1999; 99US-0164751.		
XX			
PA	(HUMA-) HUMAN GENOME SCI INC.		
XX			
PI	Ruben SM, Ni J, Komatsoulis G, Rosen CA, Soppet DR;		
XX			
DR	WPI; 2000-656322/63.		
DR	P-PSDB; AAB50393.		
XX			
PT	Uncoupling proteins and nucleic acid sequences encoding them, useful		
PT	for detecting, preventing and treating proliferative, neurological,		
PT	immune system, cardiovascular and gastrointestinal disorders -		
XX			
PT	Claim 1; Page 313-314; 343pp; English.		
XX			
CC	The present sequence is one of eighteen isolated nucleotide sequences		
CC	encoding uncoupling proteins. The nucleotide sequences may be used for		
CC	the detection of various disorders such as cancer, for chromosome		
CC	identification, as chromosome markers and for numerous other diagnostic		
CC	or research purposes. The uncoupling protein encoded by the nucleotide		
CC	sequences may be used to treat disorders such as neural, immune,		
CC	muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,		
CC	renal and proliferative disorders, wounds, infectious diseases,		
CC	thrombosis, arthritis, and infertility.		
XX			
SQ	Sequence 2876 BP; 775 A; 695 C; 669 G; 737 T; 0 other;		
	Query Match 100.0%; Score 21; DB 21; Length 2876;		
	Best Local Similarity 100.0%; Pred. No. 13;		
	Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 GCTGGCGGAGTTGGGGGCGCT 21		
DB	2734 GCTGGCGGAGTTGGGGGCGCT 2714		
RESULT 8			
ABL62379/c			
ID	ABL62379 standard; DNA; 3196 BP.		
XX			
AC	ABL62379;		
XX			
DT	15-MAY-2002 (first entry)		
XX			
DE	Colon adenocarcinoma related gene sequence SEQ ID NO:716.		
XX			
XX	Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;		
KW	stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;		
KW	cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;		
KW	gene; ds.		

XX OS Homo sapiens.
XX PN WO200194629-A2.
XX PD 13-DEC-2001.
XX PF 30-MAY-2001; 2001WO-US10838.
XX PR 05-JUN-2000; 2000US-209473P.
XX PR 05-JUN-2000; 2000US-209531P.
XX PR 18-SEP-2000; 2000US-233133P.
XX PR 18-SEP-2000; 2000US-233617P.
XX PR 20-SEP-2000; 2000US-234009P.
XX PR 20-SEP-2000; 2000US-234034P.
XX PR 20-SEP-2000; 2000US-234052P.
XX PR 22-SEP-2000; 2000US-234059P.
XX PR 22-SEP-2000; 2000US-234567P.
XX PR 22-SEP-2000; 2000US-234567P.
XX PR 25-SEP-2000; 2000US-234923P.
XX PR 25-SEP-2000; 2000US-235077P.
XX PR 25-SEP-2000; 2000US-235082P.
XX PR 25-SEP-2000; 2000US-235134P.
XX PR 25-SEP-2000; 2000US-235280P.
XX PR 26-SEP-2000; 2000US-235637P.
XX PR 26-SEP-2000; 2000US-235638P.
XX PR 27-SEP-2000; 2000US-235711P.
XX PR 27-SEP-2000; 2000US-235720P.
XX PR 27-SEP-2000; 2000US-235840P.
XX PR 27-SEP-2000; 2000US-235863P.
XX PR 28-SEP-2000; 2000US-236028P.
XX PR 28-SEP-2000; 2000US-236032P.
XX PR 28-SEP-2000; 2000US-236033P.
XX PR 28-SEP-2000; 2000US-236034P.
XX PR 28-SEP-2000; 2000US-236109P.
XX PR 28-SEP-2000; 2000US-236111P.
XX PR 29-SEP-2000; 2000US-236842P.
XX PR 29-SEP-2000; 2000US-245084P.
(AVAL-) AVALON PHARM.
XX PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
XX PI Soppet DR, Weaver Z;
XX PF WPI; 2002-198264/24.
XX PT Screening for anti-neoplastic agent involves exposing cells to a
XX PT chemical agent to be tested for anti-neoplastic activity, and
XX PT determining a change in expression of a gene of a signature gene set
XX PS Claim 1; SEQ ID 716; 44pp; English.
XX CC The present invention describes a method (M1) for screening for an
XX CC anti-neoplastic agent. The method involves exposing cells to a chemical
XX CC agent to be tested for anti-neoplastic activity, determining a change in
XX CC expression of at least one gene (I) of a signature gene set, where (I)
XX CC comprises a sequence (S) selected from 847 sequences (given in AB61664
XX CC to AB61664), or is at least 95% identical to (S), where a change in
XX CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
XX CC activity and can be used in gene therapy. M1 can be used for screening

CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilm's tumour.
XX SQ Sequence 3196 BP; 833 A; 762 C; 789 G; 812 T; 0 other;
Query Match 100.0%; Score 21; DB 24; Length 3196;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCTGGCGGAGTTGGGGGCT 21
Db 2891 GCTGGCGGAGTTGGGGGCT 2871
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ID ABL69294 standard; DNA; 3196 BP.
XX AC ABL69294;
XX DT 15-MAY-2002 (first entry)
XX DE Prostate cancer related gene sequence SEQ ID NO:7631.
XX KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
XX KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
XX KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
XX KW gene; ds.
XX OS Homo sapiens.
XX PN WO200194629-A2.
XX PD 13-DEC-2001.
XX PF 30-MAY-2001; 2001WO-US10838.
XX PR 05-JUN-2000; 2000US-209473P.
XX PR 05-JUN-2000; 2000US-209531P.
XX PR 18-SEP-2000; 2000US-233133P.
XX PR 18-SEP-2000; 2000US-233617P.
XX PR 20-SEP-2000; 2000US-234009P.
XX PR 20-SEP-2000; 2000US-234034P.
XX PR 20-SEP-2000; 2000US-234052P.
XX PR 22-SEP-2000; 2000US-234567P.
XX PR 22-SEP-2000; 2000US-234567P.
XX PR 25-SEP-2000; 2000US-234923P.
XX PR 25-SEP-2000; 2000US-235077P.
XX PR 25-SEP-2000; 2000US-235082P.
XX PR 25-SEP-2000; 2000US-235134P.
XX PR 25-SEP-2000; 2000US-235280P.
XX PR 26-SEP-2000; 2000US-235637P.
XX PR 26-SEP-2000; 2000US-235638P.
XX PR 27-SEP-2000; 2000US-235711P.
XX PR 27-SEP-2000; 2000US-235720P.
XX PR 27-SEP-2000; 2000US-235840P.
XX PR 27-SEP-2000; 2000US-235863P.
XX PR 28-SEP-2000; 2000US-236028P.
XX PR 28-SEP-2000; 2000US-236032P.
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 PR 03-OCT-2000; 2000US-237608P.
 PR 03-OCT-2000; 2000US-237608P.
 PR 01-NOV-2000; 2000US-244867P.
 PR 01-NOV-2000; 2000US-245084P.
 XX (AVAL-) AVALON PHARM.
 PA Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 PI Soppet DR, Weaver Z;
 PI WPI; 2002-188264/24.
 DR
 XX Screening for anti-neoplastic agent involves exposing cells to a
 PT chemical agent to be tested for anti-neoplastic activity, and
 PT determining a change in expression of a gene of a signature gene set -
 XX
 PS Claim 1; SEQ ID 7631; 44pp; English.
 XX
 CC The present invention describes a method (M1) for screening for an
 CC anti-neoplastic agent. The method involves exposing cells to a chemical
 CC agent to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I) of a signature gene set, where (I)
 CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
 CC to ABL70110), or is at least 95% identical to (S), where a change in
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
 CC activity and can be used in gene therapy. M1 can be used for screening
 CC an anti-neoplastic agent, and can be used for producing a product which
 CC is the data collected with respect to the anti-neoplastic agent as a
 CC result of M1, and the data is sufficient to convey the chemical
 CC structure and/or properties of the agent. M1 can be used in the
 CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
 CC esophageal, ovarian, kidney, prostate or pancreatic cancer,
 CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
 CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
 CC carcinoma, papillary carcinoma and Wilms' tumour.
 XX
 SQ Sequence 3196 BP; 833 A; 762 C; 789 G; 812 T; 0 other;
 Query Match 100.0%; Score 21; DB 24; Length 3196;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTGGCGGAGTTGGGGCCT 21
 Db 2891 GCTGGCGGAGTTGGGGCCT 2871
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 ABLN99663/c
 ID ABLN99663 standard; DNA; 8133 BP.
 XX
 AC ABLN99663;
 AC
 DT 16-AUG-2002 (first entry)
 XX
 DE Human clusterin gene sequence 2.
 XX
 KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
 KW hypercholesterolaemia; cardiovascular disorder; ds;
 KW hyperproliferative disorder; hyperlipidemic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200222635-A1.

XX 21-MAR-2002.
 PD
 XX 10-SEP-2001; 2001WO-US28235.
 PF
 XX 11-SEP-2000; 2000US-06S9791.
 PR
 XX (ISIS-) ISIS PHARM INC.
 PA Monia BP, Freier SM;
 PI WPI; 2002-404805/43.
 DR
 XX Novel antisense compound targeted to nucleic acid molecule encoding
 PT clusterin, useful for treating animal having disease associated with
 PT clusterin such as hyperlipidemic disorder, cardiovascular disorder -
 PS Example 15; Page 93-98; 125pp; English.
 XX
 CC The invention comprises antisense oligonucleotides that are capable of
 CC inhibiting expression of the human clusterin gene. The antisense
 CC oligonucleotides of the invention are useful for inhibiting the
 CC expression of clusterin in cells. The antisense oligonucleotides are also
 CC useful for treating an animal with a disease or condition associated with
 CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
 CC hyperproliferative disorders; and hyperlipidemic disorders). The present
 CC DNA sequence represents a human clusterin gene sequence.
 XX
 SQ Sequence 8133 BP; 1982 A; 2024 C; 2002 G; 2125 T; 0 other;
 Query Match 100.0%; Score 21; DB 24; Length 8133;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 RESULT 11
 ABL80072
 ID ABL80072 standard; cDNA; 250 BP.
 XX
 AC ABL80072;
 AC
 DT 17-MAY-2002 (first entry)
 XX
 DE Human ovarian cancer related cDNA clone SEQ ID NO:3050.
 XX
 KW Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200192581-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 29-MAY-2001; 2001WO-US17756.
 XX
 PR 26-MAY-2000; 2000US-207484P.
 XX
 PA (CORI-) CORIXA CORP.
 PI Algate PA, Harlocker SL, Jones R;
 PI WPI; 2002-122075/16.
 DR
 XX Composition for therapy and diagnosis of ovarian cancer comprising
 PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
 PT polypeptide, antibody specific to polypeptide or T cell expressing
 PT polypeptide -
 XX
 PS Claim 1; SEQ ID 3050; 489pp; English.

PT production of enzymes, secondary metabolites or other commercially and
 PT medically useful products -

PS Disclosure; Page 63-64; 71pp; English.

XX The present invention relates to novel fungal gene expression regulators
 CC (ABQ94217-ABQ94285 and ABP63084-ABP63152). An01, An05, An09, An10, An13,
 CC An17, An20, An28, An34, At01-2, At03, At05, At07, At08, At11,
 CC At14, At16, At18, At19, At20, At22, At24, At27, At32, Pc05, Pc06, Pc07,
 CC Pc08, Pc09, Pc10, Pc18, Pc23, Pc24, Pc25, Pc33 and Pc34 are FLO11 gene
 CC expression regulators. FLO11 is required for fungal invasion and its
 CC expression is believed to be regulated by factors that also modulate
 CC secondary metabolite production. At279, At286, At291, At320, At322,
 CC An1000, At167, At221, At233, At239, At240, At274, Pc1000 and Pc1001 are
 CC lovF gene expression regulators, and At501 and At574 are lovE gene
 CC expression regulators. lovF and lovE are believed to be involved in the
 CC production of the secondary metabolite lovastatin. Pc804 is an acvA gene
 CC expression regulator. acvA is involved in the production of the secondary
 CC metabolite penicillin. The fungal gene expression regulators and their
 CC coding sequences are useful in regulating or manipulating the expression
 CC of fungal genes that are involved in the production of enzymes, secondary
 CC metabolites and other commercially and medically useful products, in
 CC order to achieve maximum benefit. The genes may also be used to identify
 CC genes relevant to fungal invasion which may act as targets for the
 CC development of antifungal drugs.

XX SQ Sequence 3732 BP; 969 A; 1265 C; 951 G; 547 T; 0 other;

Query Match 82.9%; Score 17.4; DB 24; Length 3732;
 Best Local Similarity 94.7%; Pred. No. 3.8e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 CTGGCGCGAGTTGGGGGCC 20
 |||||
 DB 2566 CTGGCGCGAGTTGGGGGCC 2548

RESULT 14

ABZ57220

ID ABZ57220 standard; cDNA; 2137 BP.

XX AC ABZ57220;

XX 24-MAR-2003 (first entry)

DE Human zinc finger protein 11.22-encoding cDNA.

XX Human; zinc finger protein 11.22; recombinant production;
 KW gene therapy; malignant tumour; cancer; blood disease; HIV infection;
 KW human immunodeficiency virus; immune disorder; inflammatory condition;
 KW cytostatic; antiinflammatory; immunomodulator; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 6..314

FT /*tag= a

FT /product= "Human zinc finger protein 11.22"

XX CN1364797-A.

XX 21-AUG-2002.

XX 10-JAN-2001; 2001CN-0105174.

XX 10-JAN-2001; 2001CN-0105174.

XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.

XX Mao Y, Xie Y;

XX WPI; 2003-000509/01.

DR P-PSDB; ABP58706.

XX

PT New polypeptide-human zinc finger protein 11.22 and polynucleotide
 PT encoding for the polypeptide, useful for treating various diseases such
 PT as malignant tumors, hemopathy, HIV infection, immunological diseases
 PT and inflammation -

XX Claim 6; Page 25-26 (Disclosure); 33pp; Chinese.

XX The invention relates to human zinc finger protein 11.22 (ABP58706) and
 CC nucleic acids encoding it (ABZ57220). The protein has a molecular weight
 CC of 11.22 kb. The invention also relates to a method for the recombinant
 CC production of the protein, an antagonist of the protein, and the use of
 CC the protein, gene and antagonist in therapeutic applications. Zinc finger
 CC protein 11.22 can be used in the treatment of a variety of diseases such
 CC as malignant tumors, blood diseases, HIV (human immunodeficiency virus)
 CC infection, immune disorders and inflammatory conditions. The present
 CC sequence represents cDNA encoding human zinc finger protein 11.22.

XX SQ Sequence 2137 BP; 591 A; 487 C; 469 G; 590 T; 0 other;

Query Match 80.0%; Score 16.8; DB 25; Length 2137;

Best Local Similarity 90.0%; Pred. No. 6.7e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GCTGGCGCGAGTTGGGGGCC 20

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 DB 762 GCTGGCGCGAGTTGGGGGCC 781

RESULT 15

AAH25134/c

ID AAH25134 standard; DNA; 2535 BP.

XX AC AAH25134;

XX 22-AUG-2001 (first entry)

XX Nucleotide sequence of human alcohol dehydrogenase 21612.

XX Human; alcohol dehydrogenase; colon disorder; brain disorder;
 KW skin disorder; heart disorder; blood vessel disorder; kidney disorder;
 KW prostate disorder; skeletal muscle disorder; ovary disorder;
 KW testis disorder; epididymis disorder; spleen disorder; lung disorder;
 KW liver disorder; uterus disorder; endometrium disorder; T-cell disorder;
 KW red cell disorder; thymus disorder; B cell disorder; breast disorder;
 KW thyroid disorder; pancreas disorder; small intestine disorder;
 KW reduced platelet number disorder; precursor T cell neoplasm; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 762..2018

FT /*tag= a

FT /product= "alcohol dehydrogenase 21612"

XX WO200144446-A2.

XX 21-JUN-2001.

XX 15-DEC-2000; 2000WO-US33873.

XX 15-DEC-1999; 99US-0464039.

XX (MILL-) MILLENNIUM PHARM INC.

XX Meyers R;

XX WPI; 2001-390244/41.

DR P-PSDB; AAB84367.

XX Novel human alcohol dehydrogenase proteins, 21612, 21615, 21620, 21676,
 PT 33756, useful for treating psoriasis, tropical sprue, pancreatitis,
 PT goiter, osteomalacia, endometriosis, angina pectoris, embolism -

XX Claim 2; Fig 15; 156pp; English.
PS
XX AAH25131-35 encode human alcohol dehydrogenase proteins, designated
CC 21620, 33756, 21676, 21612 and 21615, respectively. Alcohol dehydrogenase
CC polynucleotides and polypeptides are useful for treatment and diagnosis
CC of disorders mediated by or related to alcohol dehydrogenase. They can
CC be used for treating disorders of colon, brain, skin, heart, blood
CC vessels, kidney, prostate, skeletal muscle, ovary, testis and epididymis,
CC spleen, lung, liver, uterus and endometrium, T-cells, red cells, thymus,
CC B cells, breast, thyroid, pancreas, small intestine, reduced platelet
CC number, precursor T cell neoplasms, bone forming cells, and bone marrow
CC cells.
XX
SQ Sequence 2535 BP; 720 A; 531 C; 537 G; 695 T; 52 other;
Query Match 80.0%; Score 16.8; DB 22; Length 2535;
Best Local Similarity 90.0%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCTGGCGGGAGTTGGGGCC 20
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41	16.4	78.1	256	9	US-09-723-835-10
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44	16.4	78.1	256	9	US-09-768-836-10
45	16.4	78.1	256	9	US-09-726-348-13

ALIGNMENTS

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; Sequence 12, Application US/09944326
; Patent No. US20020128220A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Neilson, Colleen
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY
; FILE REFERENCE: USC.P-020-2
; CURRENT APPLICATION NUMBER: US/09/944.326
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 12
; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-09-944-326-12

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Best Local Similarity 100.0%; Pred. No. 10;
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RESULT 2
US-09-967-726A-12

GenCore version 5.1.6
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SUMMARIES

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3	21	100.0	21	US-10-080-794-12	Sequence 12, Appl
C 4	21	100.0	450	US-09-918-995-759	Sequence 759, App
C 5	21	100.0	450	US-09-833-381-159	Sequence 159, App
C 6	21	100.0	1495	US-10-210-130-74	Sequence 74, Appl
C 7	21	100.0	1678	US-09-765-231A-16	Sequence 16, Appl
C 8	21	100.0	1775	US-10-133-033-43	Sequence 243, App
C 9	21	100.0	2876	US-10-118-258-17	Sequence 17, Appl
C 10	21	100.0	3196	US-09-969-708-160	Sequence 160, App
C 11	21	100.0	3196	US-09-873-367C-716	Sequence 716, App
12	19.4	92.4	403	US-09-833-381-444	Sequence 444, App
13	19.4	92.4	525	US-09-833-381-444	Sequence 444, App
C 14	19.4	92.4	4283	US-09-814-353-19511	Sequence 19511, A
C 15	18.4	87.6	2957	US-10-029-632-101667	Sequence 101667, A

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; Sequence 12, Application US/09967726A
; Publication No. US20030158130A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Zellweger, Tobias
; TITLE OF INVENTION: Chemo- and Radiation-Sensitization of Cancer by Antisense TRPM-2
; FILE REFERENCE: UBC-P-022
; CURRENT APPLICATION NUMBER: US/09/967,726A
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 12
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
; OTHER INFORMATION: antisense TRPM-2 ODN
; US-09-967-726A-12

Query Match      100.0%; Score 21; DB 13; Length 21;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Publication No. US20030166591A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY USING AN OLIGONUCLEOTIDE
; FILE REFERENCE: UBC-P-020-3
; CURRENT APPLICATION NUMBER: US/10/080,794
; CURRENT FILING DATE: 2002-02-22
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 09/944,326
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 12
; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
; US-10-080-794-12

Query Match      100.0%; Score 21; DB 13; Length 21;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCGGAGTTGGGGGCT 21
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Db 1 GCTGGCGGAGTTGGGGGCT 21

RESULT 4
US-09-918-995-759/c
; Sequence 759, Application US/09918995

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; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 759
; LENGTH: 450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(450)
; OTHER INFORMATION: n = A,T,C or G
; US-09-918-995-759

Query Match      100.0%; Score 21; DB 11; Length 450;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCGGAGTTGGGGGCT 21
   |||||
Db 303 GCTGGCGGAGTTGGGGGCT 283

RESULT 5
US-09-833-381-159
; Sequence 159, Application US/09833381
; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NO US20020132090A1el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 159
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
; US-09-833-381-159

Query Match      100.0%; Score 21; DB 10; Length 505;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCGGAGTTGGGGGCT 21
   |||||
Db 105 GCTGGCGGAGTTGGGGGCT 125

RESULT 6
US-10-210-120-74/c
; Sequence 74, Application US/10210120
; Publication No. US20030175736A1
; GENERAL INFORMATION:
; APPLICANT: Chinnaiyan, Arul M.
; APPLICANT: Ruben, Mark A.
; APPLICANT: Sreekumar, Arun
; TITLE OF INVENTION: Expression Profile of Prostate Cancer
; FILE REFERENCE: UM-07221
; CURRENT APPLICATION NUMBER: US/10/210,120
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/309,581

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/ PRIOR FILING DATE: 2001-08-02
/ PRIOR APPLICATION NUMBER: US 60/334,468
/ PRIOR FILING DATE: 2001-11-15
/ NUMBER OF SEQ ID NOS: 123
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 74
/ LENGTH: 1495
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-210-120-74

Query Match      100.0%; Score 21; DB 13; Length 1495;
Best Local Similarity 100.0%; Pred. No. 4.4; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
Db 1388 GCTGGCGGAGTTGGGGCCT 1368

RESULT 7
US-09-765-231A-16/c
/ Sequence 16, Application US/09765231A
/ Patent No. US20020119452A1
/ GENERAL INFORMATION:
/ APPLICANT: Searle/Monsanto
/ APPLICANT: Phippard, Deborah
/ APPLICANT: Vasanthakumari, Geetha
/ APPLICANT: Dotson, Stanton
/ APPLICANT: Ma, Xiao-Jun
/ TITLE OF INVENTION: Osteoarthritis tissue-derived nucleic acids, polypeptides,
/ TITLE OF INVENTION: vectors, and cells
/ FILE REFERENCE: SO-3221 PR
/ CURRENT APPLICATION NUMBER: US/09/765,231A
/ CURRENT FILING DATE: 2001-01-18
/ NUMBER OF SEQ ID NOS: 82
/ SEQ ID NO 16
/ LENGTH: 1678
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-765-231A-16

Query Match      100.0%; Score 21; DB 10; Length 1678;
Best Local Similarity 100.0%; Pred. No. 4.3; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
Db 1558 GCTGGCGGAGTTGGGGCCT 1538

RESULT 8
US-10-133-013-243/c
/ Sequence 243, Application US/10133013
/ Publication No. US2003016903A1
/ GENERAL INFORMATION:
/ APPLICANT: Astromoff, Anna
/ APPLICANT: Bandman, Olga
/ APPLICANT: Cocks, Benjamin G.
/ TITLE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE
/ FILE REFERENCE: PA-0049 US
/ CURRENT APPLICATION NUMBER: US/10/133,013
/ CURRENT FILING DATE: 2002-04-25
/ PRIOR APPLICATION NUMBER: 60/287,067
/ PRIOR FILING DATE: 2001-04-27
/ NUMBER OF SEQ ID NOS: 271
/ SOFTWARE: PERL Program
/ SEQ ID NO 243
/ LENGTH: 1775
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
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/ OTHER INFORMATION: Incyte ID No. US2003016903A1 2966620cB1
US-10-133-013-243

Query Match      100.0%; Score 21; DB 13; Length 1775;
Best Local Similarity 100.0%; Pred. No. 4.2; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
Db 1650 GCTGGCGGAGTTGGGGCCT 1630

RESULT 9
US-10-116-255-17/c
/ Sequence 17, Application US/10116255
/ Publication No. US20030036646A1
/ GENERAL INFORMATION:
/ APPLICANT: Ni et al.
/ TITLE OF INVENTION: Uncoupling Protein Polynucleotides, Polypeptides, and
/ TITLE OF INVENTION: Antibodies
/ FILE REFERENCE: PT009F1
/ CURRENT APPLICATION NUMBER: US/10/116,255
/ CURRENT FILING DATE: 2002-04-05
/ PRIOR APPLICATION NUMBER: 09/685,897
/ PRIOR FILING DATE: 2000-10-11
/ PRIOR APPLICATION NUMBER: PCT/US00/09534
/ PRIOR FILING DATE: 2000-04-06
/ PRIOR APPLICATION NUMBER: 60/128,701
/ PRIOR FILING DATE: 1999-04-09
/ PRIOR APPLICATION NUMBER: 60/142,821
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: 60/149,448
/ PRIOR FILING DATE: 1999-08-18
/ PRIOR APPLICATION NUMBER: 60/164,751
/ PRIOR FILING DATE: 1999-11-12
/ NUMBER OF SEQ ID NOS: 66
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 17
/ LENGTH: 2876
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-116-255-17

Query Match      100.0%; Score 21; DB 15; Length 2876;
Best Local Similarity 100.0%; Pred. No. 3.8; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
Db 2734 GCTGGCGGAGTTGGGGCCT 2714

RESULT 10
US-09-969-708-160/c
/ Sequence 160, Application US/09969708
/ Patent No. US20020102532A1
/ GENERAL INFORMATION:
/ APPLICANT: Augustus, Meena
/ TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Signatu
/ FILE REFERENCE: 699290-70
/ CURRENT APPLICATION NUMBER: US/09/969,708
/ CURRENT FILING DATE: 2001-10-03
/ PRIOR APPLICATION NUMBER: US/60/237,606
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: US/60/237,608
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: US/60/237,425
/ PRIOR FILING DATE: 2000-10-03
/ NUMBER OF SEQ ID NOS: 658
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 160
/ LENGTH: 3196
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-969-708-160

Query Match      100.0%; Score 21; DB 10; Length 3196;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
   |||||
Db 2891 GCTGGCGGAGTTGGGGCCT 2871

RESULT 11
US-09-873-367C-716/c
; Sequence 716, Application US/09873367C
; Publication No. US20030165839A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; APPLICANT: Soppet, Daniel
; APPLICANT: Endress, Gregory
; APPLICANT: Augustus, Mesna
; APPLICANT: Ebner, Reinhard
; APPLICANT: Carter, Kenneth
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE REFERENCE: 689290-64
; CURRENT APPLICATION NUMBER: US/09/873,367C
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: U.S. 60/236,891
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: U.S. 60/236,842
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: U.S. 60/244,867
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: U.S. 60/245,084
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 1067
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 716
; LENGTH: 3196
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-873-367C-716

Query Match      100.0%; Score 21; DB 13; Length 3196;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
   |||||
Db 2891 GCTGGCGGAGTTGGGGCCT 2871

RESULT 12
US-09-833-381-444
; Sequence 444, Application US/09833381
; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NO. US20020132090A1el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 444
; LENGTH: 403
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-444

Query Match      92.4%; Score 19.4; DB 10; Length 403;
Best Local Similarity 95.2%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
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Db 102 GCTGGCGGAGTTGGGGCCT 122

RESULT 13
US-09-833-381-443
; Sequence 443, Application US/09833381
; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NO. US20020132090A1el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 443
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-443

Query Match      92.4%; Score 19.4; DB 10; Length 525;
Best Local Similarity 95.2%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
   |||||
Db 106 GCTGGCGGAGTTGGGGCCT 126

RESULT 14
US-09-814-353-19511/c
; Sequence 19511, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-0068
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19511
; LENGTH: 4283
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-19511
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Wed Jan 21 15:56:31 2004

Query Match 92.4%; Score 19.4; DB 13; Length 4283;
Best Local Similarity 95.2%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
DB 1490 GCTGGCGGAGTTGGGGCCT 1470

RESULT 15

US-10-027-632-101667
; Sequence 101667, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101667
; LENGTH: 2257
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-101667

Query Match 87.6%; Score 18.4; DB 13; Length 2257;
Best Local Similarity 95.0%; Pred. No. 50;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCGGAGTTGGGGCCT 21
DB 1340 CTGGCTGAGTTGGGGCCT 1359

Search completed: January 21, 2004, 15:35:50
Job time : 224 secs

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OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 11:34:17 ; Search time 56 Seconds
(without alignments)
165.519 Million cell updates/sec

Title: US-09-913-325-12
Perfect score: 21
Sequence: 1 gctggcgagtggggcct 21

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/2/ina/5A-COMB.seq:
4: /cgn2_6/ptodata/2/ina/5B-COMB.seq:
5: /cgn2_6/ptodata/2/ina/PCTUS-COMB.seq:
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	21	100.0	1416	US-09-016-434-1318	Sequence 1318, Ap
C 2	21	100.0	1648	US-09-659-791A-3	Sequence 3, Appli
C 3	21	100.0	8133	US-09-659-791A-10	Sequence 10, Appl
C 4	16.8	80.0	3562	US-09-360-197-1	Sequence 1, Appli
C 5	16.8	80.0	3647	US-09-360-197-7	Sequence 7, Appli
C 6	16.4	78.1	50	US-08-171-389-590	Sequence 590, App
C 7	16.4	78.1	50	US-08-123-936-590	Sequence 590, App
C 8	16.4	78.1	50	US-08-475-228A-590	Sequence 590, App
C 9	16.4	78.1	50	US-08-482-080A-590	Sequence 590, App
C 10	16.4	78.1	50	US-09-354-947-590	Sequence 590, App
C 11	16.4	78.1	50	PCT-US93-12388-590	Sequence 590, App
C 12	16.4	78.1	68	US-08-790-963-66	Sequence 66, Appl
C 13	16.4	78.1	68	US-09-371-774-66	Sequence 66, Appl
C 14	16.4	78.1	226	US-09-659-026A-9	Sequence 9, Appli
C 15	16.4	78.1	256	US-09-106-182-24	Sequence 24, Appl
C 16	16.4	78.1	256	US-09-227-357-10	Sequence 10, Appl
C 17	16.4	78.1	256	US-09-280-839-13	Sequence 13, Appl
C 18	16.4	78.1	256	US-09-411-977-24	Sequence 24, Appl
C 19	16.4	78.1	256	US-09-479-729B-30	Sequence 30, Appl
C 20	16.4	78.1	256	US-09-257-179-10	Sequence 10, Appl
C 21	16.4	78.1	256	US-09-149-476-10	Sequence 10, Appl
C 22	16.4	78.1	256	US-09-288-143-10	Sequence 10, Appl
C 23	16.4	78.1	256	US-09-487-792-32	Sequence 32, Appl
C 24	16.4	78.1	256	US-09-152-060-10	Sequence 10, Appl
C 25	16.4	78.1	256	US-09-908-594-32	Sequence 32, Appl
C 26	16.4	78.1	256	US-09-461-325-10	Sequence 10, Appl
C 27	16.4	78.1	256	US-09-489-847-10	Sequence 10, Appl

C 28	16.4	78.1	256	4	US-09-231-788-26	Sequence 26, Appl
C 29	16.4	78.1	256	4	US-09-512-363-27	Sequence 27, Appl
C 30	16.4	78.1	256	4	US-09-176-200-27	Sequence 27, Appl
C 31	16.4	78.1	256	4	US-08-205-258-10	Sequence 10, Appl
C 32	16.4	78.1	256	4	US-09-690-454-10	Sequence 10, Appl
C 33	16.4	78.1	256	4	US-09-482-271-19	Sequence 19, Appl
C 34	16.4	78.1	256	4	US-09-482-273-10	Sequence 10, Appl
C 35	16.4	78.1	256	4	US-09-904-615-10	Sequence 10, Appl
C 36	16.4	78.1	256	4	US-09-369-247-10	Sequence 10, Appl
C 37	16.4	78.1	271	3	US-09-106-182-18	Sequence 18, Appl
C 38	16.4	78.1	271	4	US-09-227-357-5	Sequence 5, Appli
C 39	16.4	78.1	271	4	US-09-280-839-8	Sequence 8, Appli
C 40	16.4	78.1	271	4	US-09-411-977-20	Sequence 20, Appl
C 41	16.4	78.1	271	4	US-09-479-729B-25	Sequence 25, Appl
C 42	16.4	78.1	271	4	US-09-257-179-5	Sequence 5, Appli
C 43	16.4	78.1	271	4	US-09-149-476-5	Sequence 5, Appli
C 44	16.4	78.1	271	4	US-09-288-143-5	Sequence 5, Appli
C 45	16.4	78.1	271	4	US-09-487-792-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-09-016-434-1318/c
; Sequence 1318, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 895-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1318:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1416 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g338056
; US-09-016-434-1318

Query Match 100.0%; Score 21; DB 4; Length 1416;
Best Local Similarity 100.0%; Pred. No. 2.1;

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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
Db 1309 GCTGGCGGAGTTGGGGCCT 1289

RESULT 2
US-09-659-791A-3/c
; Sequence 3, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 3
; LENGTH: 1648
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (53)...(1402)
US-09-659-791A-3.

Query Match 100.0%; Score 21; DB 4; Length 1648;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
Db 1541 GCTGGCGGAGTTGGGGCCT 1521

RESULT 3
US-09-659-791A-10/c
; Sequence 10, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 10
; LENGTH: 8133
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-659-791A-10.

Query Match 100.0%; Score 21; DB 4; Length 8133;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
Db 7752 GCTGGCGGAGTTGGGGCCT 7732

RESULT 4
US-09-360-197-1/c
; Sequence 1, Application US/09360197
; Patent No. 6287859
; GENERAL INFORMATION:
; APPLICANT: Basiliana, Frederic
; APPLICANT: Lazdunski, Michel
; APPLICANT: Waldmann, Rainer
; APPLICANT: Deweille, Jan R.
```

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; TITLE OF INVENTION: Human and Rat Families of Neuronal Acid-Sensitive
; TITLE OF INVENTION: Cationic Channels, Their Cloning and Applications
; FILE REFERENCE: 989.6706P
; CURRENT APPLICATION NUMBER: US/09/360,197
; CURRENT FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: 09/129,758
; PRIOR FILING DATE: 1998-08-05
; PRIOR APPLICATION NUMBER: 60/095,408
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3562
; TYPE: DNA
; ORGANISM: rattus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (123)..(1700)
US-09-360-197-1

Query Match 80.0%; Score 16.8; DB 3; Length 3562;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGGCC 20
Db 1778 GCTGGCGGAGTTGGGGGCC 1759

RESULT 5
US-09-360-197-7/c
; Sequence 7, Application US/09360197
; Patent No. 6287859
; GENERAL INFORMATION:
; APPLICANT: Basiliana, Frederic
; APPLICANT: Lazdunski, Michel
; APPLICANT: Waldmann, Rainer
; APPLICANT: Deweille, Jan R.
; TITLE OF INVENTION: Human and Rat Families of Neuronal Acid-Sensitive
; TITLE OF INVENTION: Cationic Channels, Their Cloning and Applications
; FILE REFERENCE: 989.6706P
; CURRENT APPLICATION NUMBER: US/09/360,197
; CURRENT FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: 09/129,758
; PRIOR FILING DATE: 1998-08-05
; PRIOR APPLICATION NUMBER: 60/095,408
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 3647
; TYPE: DNA
; ORGANISM: rattus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (109)..(1785)
US-09-360-197-7

Query Match 80.0%; Score 16.8; DB 3; Length 3647;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGGCC 20
Db 1863 GCTGGCGGAGTTGGGGGCC 1844

RESULT 6
US-08-171-389-590/c
; Sequence 590, Application US/08171389
; Patent No. 5578444
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
```

APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,389
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175/G19P3
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 590:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Simian virus 40 T/t late (start
INDIVIDUAL ISOLATE: site 31)
US-08-171-389-590

Query Match 78.1%; Score 16.4; DB 1; Length 50;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTGGCGCGAGTTGGGGC 19
Db 20 CTGGCGCGAGTTAGGGGC 3

RESULT 7
US-08-123-936-590/c
Sequence 590, Application US/08123936
Patent No. 5726014
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.

TITLE OF INVENTION: Screening Assay for the Detection of
TITLE OF INVENTION: DNA-Binding Molecules
NUMBER OF SEQUENCES: 640
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,936
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0075.32/G19P2
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 590:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Simian virus 40 T/t late (start
INDIVIDUAL ISOLATE: site 31)
US-08-123-936-590

Query Match 78.1%; Score 16.4; DB 1; Length 50;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTGGCGCGAGTTGGGGC 19
Db 20 CTGGCGCGAGTTAGGGGC 3

RESULT 8
US-08-475-228A-590/c
Sequence 590, Application US/08475228A
Patent No. 5869241
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA

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; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,228A
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/123,936
; FILING DATE: 17-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/996,783
; FILING DATE: 23-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/723,618
; FILING DATE: 27-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/081,070
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 4600-0175.21/G19P3D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 590:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Simian virus 40 T/t late (start
; INDIVIDUAL ISOLATE: site 31)
; US-08-475-228A-590

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Query Match 78.1%; Score 16.4; DB 2; Length 50;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 2 CTGGCGGAGTTGGGGC 19
Db 20 CTGGCGGAGTTAGGGC 3

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RESULT 9
US-08-482-080A-590/c
; Sequence 590, Application US/08482080A
; Patent No. 6010849
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; APPLICANT: Cantor, Charles R.
; APPLICANT: Andrews, Beth M.
; APPLICANT: Turin, Lisa M.
; APPLICANT: Fry, Kirk E.
; TITLE OF INVENTION: Sequence-Directed DNA Binding
; NUMBER OF SEQUENCES: 664
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,080A
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/171,389
; FILING DATE: 20-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/123,936
; FILING DATE: 17-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/996,783
; FILING DATE: 23-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/723,618
; FILING DATE: 27-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/081,070
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Brady, John F.
; REGISTRATION NUMBER: 39,118
; REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 324-0880
; TELEFAX: (650) 324-0960
; INFORMATION FOR SEQ ID NO: 590:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Simian virus 40 T/t late (start
; INDIVIDUAL ISOLATE: site 31)
; US-08-482-080A-590

```

```

Query Match 78.1%; Score 16.4; DB 3; Length 50;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 2 CTGGCGGAGTTGGGGC 19
Db 20 CTGGCGGAGTTAGGGC 3

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RESULT 10
US-09-354-947-590/c
; Sequence 590, Application US/09354947
; Patent No. 6384208
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; APPLICANT: Cantor, Charles R.
; APPLICANT: Andrews, Beth M.
; APPLICANT: Turin, Lisa M.
; APPLICANT: Fry, Kirk E.
; TITLE OF INVENTION: Sequence-Directed DNA Binding
; NUMBER OF SEQUENCES: 664
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/354,947
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,080
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/171,389
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Brady, John F.
REGISTRATION NUMBER: 39,118
REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
TELEFAX: (650) 324-0960
INFORMATION FOR SEQ ID NO: 590:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Simian virus 40 T/t late (start
INDIVIDUAL ISOLATE: site 31)
US-09-354-947-590

Query Match 78.1%; Score 16.4; DB 4; Length 50;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCGGAGTTGGGGC 19
|||||
DB 20 CTGGCGGAGTTAGGGC 3

RESULT 11
PCT-US93-12388-590/c
Sequence 590, Application PC/TUS9312388
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Fenobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12388
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175.41/G19PCT2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 590:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Simian virus 40 T/t late (start
INDIVIDUAL ISOLATE: site 31)
PCT-US93-12388-590

Query Match 78.1%; Score 16.4; DB 5; Length 50;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCGGAGTTGGGGC 19
|||||
DB 20 CTGGCGGAGTTAGGGC 3

RESULT 12

US-08-790-963-66
Sequence 66, Application US/08790963
Patent No. 5837464
GENERAL INFORMATION:
APPLICANT: Daniel J. Capon
TITLE OF INVENTION: Compositions and Methods For
TITLE OF INVENTION: Determining Anti-viral Drug Susceptibility And
TITLE OF INVENTION: Resistance
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/790,963
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 50130-B/JPW/AKC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 base pairs

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/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
US-08-790-963-66

Query Match      78.1%; Score 16.4; DB 2; Length 68;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CTGGCGCGAGTTGGGGC 19
DB      33 CTGGCGCGAGTTAGGGC 50

RESULT 13
US-09-371-774-66
; Sequence 66, Application US/09371774
; Patent No. 6242187
; GENERAL INFORMATION:
; APPLICANT: Daniel J. Capon
; Christos John Petropoulos
; TITLE OF INVENTION: Compositions And Methods For
; Determining Anti-viral Drug Susceptibility And
; Resistance And Anti-viral Drug Screening
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version#1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/371,774
; FILING DATE: 10-Aug-1999
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50130-F/JPW/CMR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0526
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 68 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-09-371-774-66

Query Match      78.1%; Score 16.4; DB 3; Length 68;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CTGGCGCGAGTTGGGGC 19
DB      33 CTGGCGCGAGTTAGGGC 50

RESULT 14
US-09-659-026A-9/c
; Sequence 9, Application US/09659026A
; Patent No. 6461616
; GENERAL INFORMATION:
```

```
/ APPLICANT: MONTELABO, Ronald
/ APPLICANT: CRAICO, Jodi K.
/ APPLICANT: ISSEL, Charles
/ APPLICANT: PUFFER, Bridget
/ APPLICANT: HENNESSY, Kristina J.
/ APPLICANT: BROWN, Karen K.
/ TITLE OF INVENTION: EIAV P26 DELETION VACCINE AND DIAGNOSTIC
/ FILE REFERENCE: MONTELABO ET AL.
/ CURRENT APPLICATION NUMBER: US/09/659,026A
/ CURRENT FILING DATE: 2001-06-11
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 9
/ LENGTH: 226
/ TYPE: DNA
/ ORGANISM: IN VITROGEN
US-09-659-026A-9

Query Match      78.1%; Score 16.4; DB 4; Length 226;
Best Local Similarity 94.4%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CTGGCGCGAGTTGGGGC 19
DB      168 CTGGCGCGAGTTAGGGC 151

RESULT 15
US-09-106-182-24/c
; Sequence 24, Application US/09106182
; Patent No. 6046035
; GENERAL INFORMATION:
; APPLICANT: Shi, Yangu
; APPLICANT: Ruben, Steve
; TITLE OF INVENTION: Cardiostrophin-Like Cytokine
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc
; STREET: 9410 Key West Ave
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,182
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/051,053
; FILING DATE: 30-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF385
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 256 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-106-182-24

Query Match      78.1%; Score 16.4; DB 3; Length 256;
Best Local Similarity 94.4%; Pred. No. 1.6e+02;
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Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTGGGCGGAGTTGGGGC 19
| | | | | | | | | | | | | | | | | | | | | |
Db 123 CTGGGCGGAGTTAGGGC 106

Search completed: January 21, 2004, 13:11:50
Job time : 58 secs

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OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 10:59:47 ; Search time 1733 Seconds

(without alignments)
294.515 Million cell updates/sec

Title: US-09-913-325-12
Perfect score: 21
Sequence: 1 gctggggagctgggggcct 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

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- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estm:*
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- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hic:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hic:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estin:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vit:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_pig:*
- 27: em_gss_vit:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	ID	Description
1	21	100.0	121 14	H84500 yv02dd12.s1
2	21	100.0	121 14	R93611 YG38d11.s1
3	21	100.0	135 14	TS3781 YG83e02.s1
4	21	100.0	143 10	BE765434 IL3-NT010

5	21	100.0	145	10	AW904670
6	21	100.0	146	9	AA738045
7	21	100.0	150	13	BU728259
8	21	100.0	151	9	AA434384
9	21	100.0	151	12	BI055204
10	21	100.0	153	12	BI040715
11	21	100.0	157	12	BI467181
12	21	100.0	159	12	BI040516
13	21	100.0	169	9	AI523434
14	21	100.0	169	9	AI691105
15	21	100.0	171	10	BF897129
16	21	100.0	171	10	BF919288
17	21	100.0	172	9	AA235650
18	21	100.0	172	10	BF932077
19	21	100.0	174	9	AA635704
20	21	100.0	174	10	BF374244
21	21	100.0	174	10	BE702836
22	21	100.0	176	10	BF364496
23	21	100.0	176	12	BI040542
24	21	100.0	177	12	BI040538
25	21	100.0	179	10	AW868593
26	21	100.0	179	12	BI040710
27	21	100.0	181	12	BI040535
28	21	100.0	182	10	AW868587
29	21	100.0	183	14	CB048333
30	21	100.0	183	14	CB048334
31	21	100.0	184	9	AA433884
32	21	100.0	185	12	BM994290
33	21	100.0	185	14	R83374
34	21	100.0	187	10	AW897945
35	21	100.0	187	10	BE765800
36	21	100.0	187	10	BE766185
37	21	100.0	188	13	BU734617
38	21	100.0	190	10	BF749857
39	21	100.0	193	12	BI040729
40	21	100.0	195	10	AW904698
41	21	100.0	196	10	BF749861
42	21	100.0	196	12	BI040731
43	21	100.0	196	12	BI055202
44	21	100.0	198	9	AW243998
45	21	100.0	198	10	AW868592

ALIGNMENTS

RESULT 1
H84500
LOCUS
DEFINITION yv02dd12.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:241559 3' similar to gb:X14723 CLUSTERIN PRECURSOR (HUMAN);, mRNA sequence.
H84500 121 bp mRNA linear EST 13-NOV-1995
H84500.1 GI:1063171
EST.
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 121)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, N., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisan, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1

High quality sequence stops: 1
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
 Seq primer: Promega -2iml3
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES

source

1. 121
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:3790692"
 /db_xref="taxon:9606"
 /clone="IMAGE:241559"
 /sex="male"
 /dev_stage="20 week-post conception fetus"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares fetal liver spleen INFLS"
 /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
 with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
 1st strand cDNA was primed with a Pac I - oligo(dT) primer
 [5', AACTGGAAGAAATTAATAAGATCTTTTCTTTTCTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Pac I and cloned into the Pac I
 and Eco RI sites of the modified pT7T3 vector. Library
 went through one round of normalization. Library
 constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT
 ORIGIN

27 a 20 c 45 g 20 t 9 others

Query Match 100.0%; Score 21; DB 14; Length 121;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCGGAGATTGGGGCCCT 21
 |||||
 Db 95 GCTGGCGGAGATTGGGGCCCT 115

RESULT 2

R93611

LOCUS R93611 121 bp mRNA linear EST 29-AUG-1995
 DEFINITION YG38d11.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
 IMAGE:198069 3' similar to gb:X14723 CLUSTERIN PRECURSOR (HUMAN) ;
 mRNA sequence.

ACCESSION R93611

VERSION R93611.1

KEYWORDS GI:967777

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1. (bases 1 to 121)
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman,
 M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
 Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston,
 R., Williamson, A., Wohlmann, P., and Wilson, R.
 The WashU-Merck EST Project

TITLE

JOURNAL

COMMENT

Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Insert Size: 1368

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Insert Length: 1368 Std Error: 0.00

FEATURES

source

Seq primer: Promega -2iml3
 High quality sequence stop: 1.
 Location/Qualifiers
 1. 121
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:3767119"
 /db_xref="taxon:9606"
 /clone="IMAGE:198069"
 /sex="male"
 /dev_stage="20 week-post conception fetus"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares fetal liver spleen INFLS"
 /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
 with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
 1st strand cDNA was primed with a Pac I - oligo(dT) primer
 [5', AACTGGAAGAAATTAATAAGATCTTTTCTTTTCTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Pac I and cloned into the Pac I
 and Eco RI sites of the modified pT7T3 vector. Library
 went through one round of normalization. Library
 constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT
 ORIGIN

23 a 22 c 50 g 23 t 3 others

Query Match 100.0%; Score 21; DB 14; Length 121;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCGGAGTTGGGGCCCT 21
 |||||
 Db 85 GCTGGCGGAGTTGGGGCCCT 105

RESULT 3

TS3781

LOCUS

DEFINITION

TS3781 135 bp mRNA linear EST 06-FEB-1995
 YB83e02.s1 Stratagene liver (#937224) Homo sapiens cDNA clone
 IMAGE:77786 3' similar to gb:X14723 CLUSTERIN PRECURSOR
 (HUMAN), mRNA sequence.

ACCESSION TS3781

VERSION TS3781.1

KEYWORDS GI:655642

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chisapelli, B.,
 Chisoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins,
 M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore,
 B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
 Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,
 Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
 Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

8889549
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Insert Size: 1905

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LLNL This clone is available royalty-free

through LLNL; contact the IMAGE Consortium (info@image.llnl.gov)

for further information. Trace considered overall poor quality

Insert Length: 1905 Std Error: 0.00

Seq primer: -2iml3

High quality sequence stop: 1.

Location/Qualifiers

```

source
1. .135
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:77786"
/sex="male"
/dev_stage="49 years old"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene liver (#937224)"
/note="Organ: liver; Vector: pBluescript SK; Site 1: EcoRI
Site 2: XhoI; Cloned unidirectionally. Primer: Oligo
dr. Hepatectomy from normal male caucasian. Average insert
size: 1.1 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5'
GAATTCGGCAGCAG 3' -3' adaptor sequence: 5'
CTCGAGTGTGTGTGTGTGTGT 3'"
BASE COUNT      30 a   23 c   48 g   32 t   2 others
ORIGIN

Query Match      100.0%; Score 21; DB 14; Length 135;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
|||||
Db 110 GCTGGCGGAGTTGGGGCCT 130

RESULT 4
BE765434/c
LOCUS
DEFINITION IL3-NT0104-200500-144-G04 NT0104 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE765434
VERSION BE765434.1 GI:10195358
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 143)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=IL3-NT0104-200
500-144-G04&t3=2000-05-20&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 8
High quality sequence stop: 143.
Location/Qualifiers
1. .143
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NT0104"

FEATURES
source
/note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      27 a   65 c   28 g   23 t
ORIGIN

Query Match      100.0%; Score 21; DB 10; Length 143;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
|||||
Db 102 GCTGGCGGAGTTGGGGCCT 82

RESULT 5
AW904670
LOCUS
DEFINITION RCI-NN1062-260400-011-a09 NN1062 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW904670
VERSION AW904670.1 GI:8068784
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 145)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RCI-NN1062-260
400-011-a09&t3=2000-04-26&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 34
High quality sequence stop: 145.
Location/Qualifiers
1. .145
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NN1062"
/note="Organ: nervous normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      20 a   31 c   61 g   33 t
ORIGIN

```

Query Match 100.0%; Score 21; DB 10; Length 145;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCGGAGTTGGGGCCT 21
 |||||
 Db 50 GCTGGCGGAGTTGGGGCCT 70

RESULT 6
 AA738045 146 bp mRNA linear EST 22-JAN-1998
 LOCUS nx15f08.s1 NCI CGAP GC3 Homo sapiens cDNA clone IMAGE:1256199 3'
 DEFINITION similar to gb:U14723 CLUSTERIN PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION AA738045
 VERSION AA738045
 KEYWORDS EST.
 SOURCE AA738045.1 GI:2768802
 ORGANISM Homo sapiens (human)

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 JOURNAL 1 (bases 1 to 146)
 COMMENT NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-rc@mail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 CDNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Insert Length: 867 Std Error: 0.00
 Seq primer: -40ml3 fwd. RT from Amersham
 High quality sequence stop: 1.

FEATURES
 source Location/Qualifiers
 1..146
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1256199"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP GC3"
 /notes="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; 1st strand cDNA was prepared from 3 pooled
 germ cell tumors, and was then primed with a Not I -
 oligo(dT) primer. Double-stranded cDNA was ligated to Eco
 RI adaptors (Pharmacia), digested with Not I and cloned
 into the Not I and Eco RI sites of the modified pT73
 vector. Library is not normalized. Library was
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 32 a 26 c 54 g 34 t
 ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 145;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCGGAGTTGGGGCCT 21
 |||||
 Db 106 GCTGGCGGAGTTGGGGCCT 126

RESULT 7
 BU728259

LOCUS BU728259 150 bp mRNA linear EST 09-OCT-2002
 DEFINITION UI-E-CQ0-adv-g-07-0-UI.s1 UI-E-CQ0 Homo sapiens cDNA clone
 UI-E-CQ0-adv-g-07-0-UI 3', mRNA sequence.

ACCESSION BU728259
 VERSION BU728259.1 GI:23649959
 KEYWORDS EST.
 SOURCE BU728259.1
 ORGANISM Homo sapiens (human)

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 JOURNAL 1 (bases 1 to 150)
 MEDLINE Bonaldo, M.F., Lennon, G. and Soares, M.B.
 PUBMED Normalization and subtraction: two approaches to facilitate gene
 discovery
 97044477
 COMMENT Genome Res. 6 (9), 791-806 (1996)
 8889548
 Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: bento-soares@uiowa.edu
 Tissue Procurement: Dr. Gregg Hageman
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).
 Seq primer: M13 FORWARD
 PolyA=ves.

FEATURES
 source Location/Qualifiers
 1..150
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-E-CQ0-adv-g-07-0-UI"
 /dev_stage="adult"
 /tissue_type="optic nerve"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-E-CQ0"
 /note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 UI-E-CQ0 is a cDNA library containing the following
 tissue(s): optic nerve. The library was constructed
 according to Bonaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an EcoR I adaptor, digested
 with Not I, and cloned directionally into pT73-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tag for this library is CCATTAGTC. This library
 was created for the program, Gene Discovery in the Visual
 System, supported by National Eye Institute (NEI).
 TAG LIB=UI-E-CQ0
 TAG_TISSUE=human optic nerve
 TAG_SEQ=CCATTAGTC"

BASE COUNT 31 a 24 c 47 g 48 t
 ORIGIN

Query Match 100.0%; Score 21; DB 13; Length 150;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCGGAGTTGGGGCCT 21
 |||||
 Db 126 GCTGGCGGAGTTGGGGCCT 146

RESULT 8

AA434384
LOCUS zw31h1.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
DEFINITION IMAGE:770949 3' similar to gb:U14723 CLUSTERIN PRECURSOR (HUMAN);
mRNA sequence.

ACCESSION AA434384.1 GI:2139298
VERSION AA434384
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 151)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Stepien, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R., and Wilson, R.
WashU-Merck EST Project 1997
Unpublished

TITLE Contact: Wilson RK
JOURNAL Washington University School of Medicine
COMMENT 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41m3 fwd. ET from Amersham.

FEATURES
source
1..151
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5980822"
/db_xref="taxon:9606"
/clone="IMAGE:770949"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="PH10B (ampicillin resistant)"
/clone_lib="Soares ovary tumor NbHOT"
/note="Organ: ovary; Vector: pT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' TGTTACCATCTGAGTGGGACGCGGTTTCTTTTCTTTTCTTTT 3'), double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 32 a 27 c 56 g 36 t
ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 151;
Best Local Similarity 100.0%; Pred. NO. 5.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
|||||
Db 107 GCTGGCGGAGTTGGGGCCT 127

RESULT 9
LOCUS BI055204 151 bp mRNA linear EST 15-JUN-2001
DEFINITION PM2-GN0495-050201-001-905 GN0495 Homo sapiens cDNA, mRNA sequence.
ACCESSION BI055204
VERSION BI055204.1 GI:14462734
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 151)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

AA434384 151 bp mRNA linear EST 29-MAY-1997
zw31h1.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
DEFINITION IMAGE:770949 3' similar to gb:U14723 CLUSTERIN PRECURSOR (HUMAN);
mRNA sequence.

ACCESSION AA434384.1 GI:2139298
VERSION AA434384
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 151)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Stepien, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R., and Wilson, R.
WashU-Merck EST Project 1997
Unpublished

TITLE Contact: Wilson RK
JOURNAL Washington University School of Medicine
COMMENT 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41m3 fwd. ET from Amersham.

FEATURES
source
1..151
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5980822"
/db_xref="taxon:9606"
/clone="IMAGE:770949"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="PH10B (ampicillin resistant)"
/clone_lib="Soares ovary tumor NbHOT"
/note="Organ: ovary; Vector: pT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' TGTTACCATCTGAGTGGGACGCGGTTTCTTTTCTTTTCTTTT 3'), double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 32 a 27 c 56 g 36 t
ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 151;
Best Local Similarity 100.0%; Pred. NO. 5.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
|||||
Db 107 GCTGGCGGAGTTGGGGCCT 127

RESULT 9
LOCUS BI055204 151 bp mRNA linear EST 15-JUN-2001
DEFINITION PM2-GN0495-050201-001-905 GN0495 Homo sapiens cDNA, mRNA sequence.
ACCESSION BI055204
VERSION BI055204.1 GI:14462734
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 151)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
200202663
MEDLINE
10737800
PUBMED
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=PM2&t2=PM2-GN0495-050201-001-905&t3=2001-02-05&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 7
High quality sequence stop: 148.

FEATURES

source

1..151
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev stage="Adult"
/clone_lib="GN0495"
/note="Organ: placenta normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning PCR products derived from ORFEST PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT

ORIGIN

Query Match 100.0%; Score 21; DB 12; Length 151;
Best Local Similarity 100.0%; Pred. NO. 5.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
|||||
Db 61 GCTGGCGGAGTTGGGGCCT 81

RESULT 10

LOCUS

BI040715 153 bp mRNA linear EST 14-JUN-2001
PM2-NT0232-120201-005-d02 NT0232 Homo sapiens cDNA, mRNA sequence.

DEFINITION

ACCESSION

VERSION

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 153)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

MEDLINE

TITLE

JOURNAL

COMMENT

PUBMED
COMMENT

10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=PM2&t2=PM2-NT0232-
120201-005-402&t3=2001-02-12&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 34
High quality sequence stop: 153.

FEATURES
source

1..153
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="NT0232"
/notes="Organ: nervous tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research).
Profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
17 a 36 c 67 g 33 t

BASE COUNT
ORIGIN

Query Match 100.0%; Score 21; DB 12; Length 153;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
|||||
Db 35 GCTGGCGGAGTTGGGGCCT 55
|||||

RESULT 11
BI0467181
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

BI0467181
ic19a12.x4 HR85 islet Homo sapiens cDNA 3', mRNA sequence.
BI0467181
EST.
EST. 15280059
GI:15280059

Hom sapiens (human)
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 157)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hiller, L., Marra, M., Pape, D., Wyllie, T., Martin, J., Blisstein, A.,
Schmitt, A., Theising, B., Ritter, E., Rorko, I., Bennett, J., Cardenas
M., Gibbons, M., McCann, R., Cole, R., Tsagaris, R., Williams, T.,
Jackson, Y., and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished
Other_ests: ic19a12.y3
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohph.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on

obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
High quality sequence stop: 142.

FEATURES
source

1..157
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/notes="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

BASE COUNT 35 a 28 c 56 g 38 t

ORIGIN

Query Match 100.0%; Score 21; DB 12; Length 157;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
|||||
Db 104 GCTGGCGGAGTTGGGGCCT 124
|||||

RESULT 12
BI040516
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

BI040516
PM2-NT0232-070201-004-c03 NT0232 Homo sapiens cDNA, mRNA sequence.
BI040516
EST.
EST. 14447142
GI:14447142

Hom sapiens (human)
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 159)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
PUBMED
COMMENT

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=PM2&t2=PM2-NT0232-
070201-004-c03&t3=2001-02-07&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 15
High quality sequence stop: 158.

FEATURES
source

1..159
/organism="Homo sapiens"


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/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="adult"
/clone_lib="NT0232"
/notes="Organ: nervous tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      31 a  61 c  29 t      1 others
ORIGIN

Query Match      100.0%; Score 21; DB 12; Length 159;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGGCT 21
|||||
Db 134 GCTGGCGGAGTTGGGGGCT 114

RESULT 13
LOCUS      AI523434
DEFINITION ar72h08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone
IMAGE:2128191.3' similar to gb:X14723 CLUSTERIN PRECURSOR (HUMAN);,
mRNA sequence.
ACCESSION  AI523434
VERSION     AI523434.1 GI:4437569
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 169)
AUTHORS   Hallier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
JOURNAL    Unpublished
WashU-NCI Human EST Project
TITLE      Unpublished
COMMENT    Contact: wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL: contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gbco.
FEATURES             source
1..169
Location/Qualifiers
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2128191"
/sex="male"
/dev_stage="adult, age 64"
/lab_host="DH10B (phage resistant)"
/clone_lib="Barstead aorta HPLRB6"
/notes="Organ: aorta; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTAGATCTCAAGTCGAGCGCGCGCCCTTTTCTTTTCTTTTCTTTTCTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[5' AATTGATCGAAC 3' and 5' GTTGGACGG 3'], digested
with Not I and cloned into the Not I and Eco RI sites of
the modified pT73 vector. Library constructed by Bob
Barstead."
BASE COUNT      36 a  33 c  59 g  41 t
ORIGIN

Query Match      100.0%; Score 21; DB 12; Length 159;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGGCT 21
|||||
Db 134 GCTGGCGGAGTTGGGGGCT 114

RESULT 14
LOCUS      AI691105
DEFINITION tx90901.x1 NCI CGAP Ut4 Homo sapiens cDNA clone IMAGE:2276880 3'
similar to gb:X14723 CLUSTERIN PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION  AI691105
VERSION     AI691105.1 GI:4902407
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 169)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL    Unpublished
COMMENT    Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 869 Std Error: 0.00
Seq primer: -40UP from Gbco.
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/lab_host="DH10B"
/clone_lib="NCI CGAP Ut4"
/notes="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.48 kb. Life Technologies catalog #:
11542-016"
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ORIGIN

Query Match      100.0%; Score 21; DB 9; Length 169;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGGCT 21
|||||
Db 140 GCTGGCGGAGTTGGGGGCT 160

RESULT 15
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DEFINITION IL0-MT0215-281100-501-all MT0215 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BF897129
VERSION     BF897129.1 GI:12288588
KEYWORDS   EST.
SOURCE     Homo sapiens (human)

```

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1. (bases 1 to 171)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.J.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=IL0&t2=IL0-MT0215-
 281100-501-all&t3=2000-11-28&t4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 171.
 Location/Qualifiers
 1. .171
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon|9606"
 /dev_stage="Adult"
 /clone_lib="MT0215"
 /note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2:
 SmaI; A mini-library was made by cloning products derived
 from ORFESTES PCR (U.S. Letters Patent application No. 196
 ,716 - Ludwig Institute for Cancer Research) profiles
 into the puc 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."
 BASE COUNT 32 a 43 c 62 g 34 t
 ORIGIN
 Query Match 100.0%; Score 21; DB 10; Length 171;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTGGCGGAGTTGGGGGCT 21
 Db 21 GCTGGCGGAGTTGGGGGCT 41
 Search completed: January 21, 2004, 13:09:47
 Job time : 1739 secs